

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company
 Pioneer Hi-Bred International, Inc.

<120> Auxin Transport Proteins

<130> BB1355

<140>
 <141>

<150> 60/133,040
 <151> 1999-05-07

<160> 48

<170> Microsoft Office 97

<210> 1
 <211> 629
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (413)

<220>
 <221> unsure
 <222> (466)

<220>
 <221> unsure
 <222> (526)

<220>
 <221> unsure
 <222> (535)

<220>
 <221> unsure
 <222> (549)

<220>
 <221> unsure
 <222> (560)

<220>
 <221> unsure
 <222> (601)..(602)..(603)

<220>
 <221> unsure
 <222> (628)

<400> 1
 gctaaaattg ctaatatitc tccaaaggaa acaagatata taatgtttat cttcagacag 60
 catgaagcaa gataagatat atatatatcg attcttcgac cgcagtcagc atgtttgaca 120
 gatcgcaatg cctcaactcac tgaatcactg aatagatcgc tgcgctcgga gctatctttc 180

gtttccctac ctaagctaata agtaatcgct aatgctcatc agaaatttca tgtggggccg 240
 atacaccaca gcatggcgcc ttccgcacgc tgaagaagcg agcgagagag gctcacagcc 300
 ccagcaagat gtagtagacc aggggtgatgg gcagagcgat gagcatcccg aagatcacgg 360
 ctgtgctcag gatgtcggga tgaacgccgt actccttggg cgaacacgaa cngncacgat 420
 cccctgaggc agagcagcct ggacgatggc gatgtggagg aggagnccgc cagaccgacg 480
 gcgatggaag cggcggccat gaccgcgggg gctgcgaaga aaccgnacgc ccatngcgat 540
 ggccgcccanc ttgttcccgn aagcgatgat cctcgggtgc agcgccatga acaggcctag 600
 nnngaacatg gccatccgag accgcgtnc 629

<210> 2
 <211> 171
 <212> PRT
 <213> Zea mays

<400> 2
 Pro Leu Ala Ile Pro Pro Ala Gly Val Met Thr Arg Leu Ile Leu Ile
 1 5 10 15
 Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu
 20 25 30
 Ile Gly Val Val Trp Ser Leu Val Ser Tyr Arg Trp Gly Ile Glu Met
 35 40 45
 Pro Ala Ile Ile Ala Arg Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu
 50 55 60
 Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg
 65 70 75 80
 Ile Ile Ala Cys Gly Asn Lys Leu Ala Ala Ile Ala Met Gly Val Arg
 85 90 95
 Phe Val Ala Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala Val Gly
 100 105 110
 Leu Arg Gly Val Leu Leu His Ile Ala Ile Val Gln Ala Ala Leu Pro
 115 120 125
 Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Gly Val His Pro
 130 135 140
 Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala Leu Pro
 145 150 155 160
 Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu
 165 170

<210> 3
 <211> 1088
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (110)

<400> 3
 gggacgggaa agccgcggcg gcgggcgggg accccagcac ggtggccgcg ccgacggcga 60
 tgccgccgac gagcgtcatg acccggtga tcctgatcat ggtgtggcgn caactcatcc 120

WO 00/68389

PCT/US00/12061

```

gcaacccaaa cacctactcc agcctcatcg gcgtcatctg gtcgctcgtc tgcttcaggt 180
ggaacttcca gatgccggcc atcgtcctgc agtccatctc catcctgtcg gacgcggggc 240
tcgggatggc catgttcagt ctcggtgtgt tcatggcgct gcagccgcgg atcatcgct 300
gcgggaacaa ggtggcgacg ttcgccatgg cgggtgcgctt cctgaccggt ccggcggtta 360
tggcgccgcg gtccttcgcc gtgggacctc gcggcacgct tctgcacgtc gccatcgctc 420
aggcagctct gcctcagggc attgtcccct tcgtcttcgc aaaggagtac aacgtgcacc 480
ctgacattct cagcaccgca gtcatttttg gcatgtcat cgccctgccg atcacgtcg 540
tctactacat cctgctcggc ctgtgaccga cccgtgggtg atggcaatgg catgccccgc 600
attgctgtaa ctgtaaagac cgctgctgcc actttccggt caagggaggc aagtgaggag 660
actgtctgct acgacatttg cttggcgctt caaaaatgag tggcttggtt ctctctctct 720
tctatctatt ttttattttt tctctagaag taggtgtgag gattgtatgg atggaaagtg 780
tgggaggtgg acaagtcgcg gtagctaggt aggacgacaa tgggtgaggca aaacggacca 840
aaaggaggtg caagtacaaa agcttgaagg gaacaggaga tccagtttaa gcacgtcacg 900
ggatgggttg gatatttcaa cgggttcagg gtattttggt tggctgcgct gaccgatgta 960
aatcagcgc gccattgtga caggagatcg atcttgcttg agataaacag ctcacctccg 1020
gagtttgatg gcttgagata agggctcaac tcaaaaataga cagaaatata taccgtattt 1080
gtcactga
1088

```

<210> 4
 <211> 187
 <212> PRT
 <213> Zea mays

<400> 4

```

Asp Gly Lys Ala Ala Ala Ala Gly Gly Asp Pro Ser Thr Val Ala Ala
 1          5          10          15

Pro Thr Ala Met Pro Pro Thr Ser Val Met Thr Arg Leu Ile Leu Ile
          20          25          30

Met Val Trp Arg Gln Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu
          35          40          45

Ile Gly Val Ile Trp Ser Leu Val Cys Phe Arg Trp Asn Phe Gln Met
          50          55          60

Pro Ala Ile Val Leu Gln Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu
          65          70          75          80

Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg
          85          90          95

Ile Ile Ala Cys Gly Asn Lys Val Ala Thr Phe Ala Met Ala Val Arg
          100          105          110

Phe Leu Thr Gly Pro Ala Val Met Ala Ala Ala Ser Phe Ala Val Gly
          115          120          125

Leu Arg Gly Thr Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro
          130          135          140

Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro
          145          150          155          160

Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala Leu Pro
          165          170          175

Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu
          180          185

```

WO 00/68389

PCT/US00/12061

<210> 5
 <211> 253
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (150)

<220>
 <221> unsure
 <222> (164)

<220>
 <221> unsure
 <222> (194)

<220>
 <221> unsure
 <222> (229)

<220>
 <221> unsure
 <222> (237)

<220>
 <221> unsure
 <222> (240)

<400> 5
 gccccacccc actcatcaca ctctcccacc gcacctcgcc gccgcggggc accgcgccat 60
 aaagtgcgtt cccggcctgc acggacgtcg aggagcagct cgcaagtgtt tcttgggtgcg 120
 tcgatcggca agatgatcac cggcacggan cttctaccac gtcntgacgg ccatgggtgcc 180
 gttgtacgtt gccntgatcc tggcgtacgg atccgtcagg tggtggcgna tcttcangcn 240
 gggaccagtg ctc 253

<210> 6
 <211> 31
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (3)

<220>
 <221> UNSURE
 <222> (8)

<220>
 <221> UNSURE
 <222> (18)

<400> 6
 Ala Arg Xaa Phe Tyr His Val Xaa Thr Ala Met Val Pro Leu Tyr Val
 1 5 10 15
 Ala Xaa Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Arg Ile Phe
 20 25 30

<210> 7
<211> 624
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (48) .. (49)

<220>
<221> unsure
<222> (51) .. (52)

<220>
<221> unsure
<222> (99)

<220>
<221> unsure
<222> (102) .. (103)

<220>
<221> unsure
<222> (107) .. (108)

<220>
<221> unsure
<222> (112)

<220>
<221> unsure
<222> (114)

<220>
<221> unsure
<222> (116)

<220>
<221> unsure
<222> (118)

<220>
<221> unsure
<222> (129)

<220>
<221> unsure
<222> (137)

<220>
<221> unsure
<222> (389)

<220>
<221> unsure
<222> (444)

<220>
<221> unsure
<222> (456)

<220>
 <221> unsure
 <222> (490)

<220>
 <221> unsure
 <222> (555)

<220>
 <221> unsure
 <222> (622)

<400> 7
 ggatggtcca aggagagctt ggggctcgct gccacctcgc gcgccagnnc nnaaataaat 60
 cactcccacg cacaccacc accgcgcgca gcacctccnc cnncccncc tncncncc 120
 caccctccnc actagcncta tctagctgag tgaactgaac agcccactgg ctctgtcttag 180
 ctaagctcag ctgtaaagct aagggttcgga gtagctagcg tgggtggccg agagtgtagc 240
 gagcggcgtt cagctcaccg ggggctgctg ggtgagttag ggaaccagcg tcgtgagagc 300
 gctccaagat gattacgggg acggacttct accacgtcat gacggccgtg gtgccgctgt 360
 acgtggcgat gatcctggcc tacgggtcng tgcggtggtg gcgcattctt tcgccggaac 420
 aatgctccgg gatcaaccgc ttctntggcg tcttcncggt gccgctgctg tccttccact 480
 tcatctccan caacaaccct acaccatgaa cctgcgcttc atcgccgccg aaacctggca 540
 aaactcatgg tgctnngcat gctcaccgcg tggaaccact caacgccggg ggaacctgga 600
 aattgaacat caagctcttc tnc 624

<210> 8
 <211> 78
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (46)

<220>
 <221> UNSURE
 <222> (50)

<220>
 <221> UNSURE
 <222> (61)

<400> 8
 Met Ile Thr Gly Thr Asp Phe Tyr His Val Met Thr Ala Val Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Arg
 20 25 30
 Ile Phe Ser Pro Glu Gln Cys Ser Gly Ile Asn Arg Phe Xaa Ala Leu
 35 40 45
 Phe Xaa Val Pro Leu Leu Ser Phe His Phe Ile Ser Xaa Gln Gln Pro
 50 55 60
 Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Glu Thr Trp Gln
 65 70 75

<210> 9
 <211> 1426
 <212> DNA
 <213> Zea mays

<400> 9
 ccacgcgtcc gggatggtcc aaggagagct tggggctcgc tgccacctcg cgcgccagcg 60
 cctaaataaa tcaactccac gcacacccac caccgcgccg agcacctcct ccttcccttc 120
 cttctctctc ccaccctcct cactagctct atctagctga gtgaactgaa cagcccactg 180
 gctcgtctta gctaagctca gctgtaaagc taaggttcgg agtagctagc gtggtggccg 240
 gagagtgtag cgagcggcgt tcagctcacc gggggctgct ggggtgagtga gggaaccagc 300
 gtcgtgagag cgctccaaga tgattacggg gacggacttc taccacgtca tgacggccgt 360
 ggtgccgctg tacgtggcga tgatcctggc ctacgggtcg gtgcggtggt ggcgcattct 420
 ctgcgccgac cagtgtctcg ggatcaaccg cttcgtggcg ctcttcgcgg tgccgctgct 480
 gtccttccac ttcattctca ccaacaaccc ctacaccatg aacctgcgt tcatcgccgc 540
 cgacacgctg cagaagctca tgggtgctggc catgctcacc gcgtggagcc acctcagccg 600
 ccggggcagc ctggagtga ccatcacgct cttctccctc tccacgctgc ccaacacgct 660
 cgtcatgggc atccccctgc tcaagggcgt gtacggcgac ttctccggca gcctcatggt 720
 gcagatcgct gtgtccagt gcatcatctg gtacacgctc atgctcttca tggtcgagta 780
 ccgcggcgcg cggatgctca tcaccgagca gttcccggac aacgcggggg ccatcgccctc 840
 catcgctcgtc gacccggagc tgggtctcct cgacggccgc agggacgcca tcgagacgga 900
 ggccgaggtc aaggaggacg gcaggatata cgtcacctg cgccgctcca acgcctcgcg 960
 ctccgacatc tactcgcgcc gctccatggg cttctccagc accacgccgc gccccagcaa 1020
 cctgaccaac gccgagatct actcgtgca gtcgtcgcgc aacccgaccc cgcggggctc 1080
 cagcttcaac cacaacgact tctactccat ggtcggccgc agctccaact tcggcgcggc 1140
 cgacgcgttc ggcattccga ccggcgccac gccgcgcccg tccaactacg aggacgacgc 1200
 gtccaagccc aagtaccctc tcccgtggt gaatgcgacg tccggggcgg gggcggtca 1260
 ctaccccgcg ccgaaccg cggtggccgc ggcgccaaag ggcgccagga aggcggcgac 1320
 gaacgggcag gccaaaggcg aggacctcca catgttcgtc tggagctcca gcgcgtcgcc 1380
 cgtgtcggac gtcttcggcg gtggcgcccc ggactacaac gaggcc 1426

<210> 10
 <211> 369
 <212> PRT
 <213> Zea mays

<400> 10
 Met Ile Thr Gly Thr Asp Phe Tyr His Val Met Thr Ala Val Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Arg
 20 25 30
 Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro
 50 55 60
 Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Leu
 65 70 75 80
 Met Val Leu Ala Met Leu Thr Ala Trp Ser His Leu Ser Arg Arg Gly
 85 90 95
 Ser Leu Glu Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asp Phe
 115 120 125

Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp
 130 135 140
 Tyr Thr Leu Met Leu Phe Met Phe Glu Tyr Arg Gly Ala Arg Met Leu
 145 150 155 160
 Ile Thr Glu Gln Phe Pro Asp Asn Ala Gly Ala Ile Ala Ser Ile Val
 165 170 175
 Val Asp Pro Asp Val Val Ser Leu Asp Gly Arg Arg Asp Ala Ile Glu
 180 185 190
 Thr Glu Ala Glu Val Lys Glu Asp Gly Arg Ile His Val Thr Val Arg
 195 200 205
 Arg Ser Asn Ala Ser Arg Ser Asp Ile Tyr Ser Arg Arg Ser Met Gly
 210 215 220
 Phe Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile
 225 230 235 240
 Tyr Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe
 245 250 255
 Asn His Asn Asp Phe Tyr Ser Met Val Gly Arg Ser Ser Asn Phe Gly
 260 265 270
 Ala Ala Asp Ala Phe Gly Ile Arg Thr Gly Ala Thr Pro Arg Pro Ser
 275 280 285
 Asn Tyr Glu Asp Asp Ala Ser Lys Pro Lys Tyr Pro Leu Pro Val Val
 290 295 300
 Asn Ala Thr Ser Gly Ala Gly Ala Ala His Tyr Pro Ala Pro Asn Pro
 305 310 315 320
 Ala Val Ala Ala Ala Pro Lys Gly Ala Arg Lys Ala Ala Thr Asn Gly
 325 330 335
 Gln Ala Lys Gly Glu Asp Leu His Met Phe Val Trp Ser Ser Ser Ala
 340 345 350
 Ser Pro Val Ser Asp Val Phe Gly Gly Gly Ala Pro Asp Tyr Asn Glu
 355 360 365

Ala

<210> 11
 <211> 504
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (126)

WO 00/68389

PCT/US00/12061

<220>
 <221> unsure
 <222> (192)

<220>
 <221> unsure
 <222> (205)

<220>
 <221> unsure
 <222> (237)

<220>
 <221> unsure
 <222> (242)

<220>
 <221> unsure
 <222> (244)

<220>
 <221> unsure
 <222> (255)

<220>
 <221> unsure
 <222> (258)

<220>
 <221> unsure
 <222> (263)

<220>
 <221> unsure
 <222> (265)

<220>
 <221> unsure
 <222> (287)

<220>
 <221> unsure
 <222> (430)

<220>
 <221> unsure
 <222> (449)

<220>
 <221> unsure
 <222> (455)

<220>
 <221> unsure
 <222> (488)

<220>

<221> unsure

<222> (490)

<400> 11

```

ttttttgagc cctacaacca ctctcttctt cattgctcca cactaccatc tcattctctcc 60
gccattttac accactccct tctcgttgca acccaacaaa ttggcactgc tcgtcgccga 120
ccccnctcc ctccccgctg cccccgacaa gccatccgcg gccatgatca ccgcgctgga 180
cctctaccac gngctgacgg ctggnggtgc cgctgtacgt ggccatgacg ctggcgcnacg 240
gntnecgtccg ctggngnggc atntncacgc cggaccagtg ctccggnatc aaccgcttcg 300
tggcgctctt cgccgtgccc ctctctctct tccacttcat ctccaccaac gacccttcg 360
ccatgaacct gcgcttcctg gccgtcgaca cgctgcagaa ggtggccgct ctcgcgctgc 420
tggcgctggn ctcccgcggc ctcttctcnc cgagngcgct cagggtcga ctggagcatc 480
aagctctncn ccctctccac gctc

```

504

<210> 12

<211> 114

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (10)

<220>

<221> UNSURE

<222> (14)

<220>

<221> UNSURE

<222> (25)

<220>

<221> UNSURE

<222> (27)

<220>

<221> UNSURE

<222> (31) .. (32) .. (33) .. (34)

<220>

<221> UNSURE

<222> (89)

<220>

<221> UNSURE

<222> (91)

<220>

<221> UNSURE

<222> (96)

<220>

<221> UNSURE

<222> (98)

<220>
 <221> UNSURE
 <222> (109)..(110)

<400> 12

Met Ile Thr Ala Leu Asp Leu Tyr His Xaa Leu Thr Ala Xaa Val Pro
 1 5 10 15

Leu Tyr Val Ala Met Thr Leu Ala Xaa Gly Xaa Val Arg Trp Xaa Xaa
 20 25 30

Xaa Xaa Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
 50 55 60

Phe Ala Met Asn Leu Arg Phe Leu Ala Val Asp Thr Leu Gln Lys Val
 65 70 75 80

Ala Val Leu Ala Leu Leu Ala Leu Xaa Ser Xaa Ala Ala Ser Ser Xaa
 85 90 95

Arg Xaa Arg Ser Gly Leu Asp Trp Ser Ile Lys Leu Xaa Xaa Leu Ser
 100 105 110

Thr Leu

<210> 13
 <211> 2769
 <212> DNA
 <213> Zea mays

<400> 13

ccacgcgtcc	gctgagccct	acaaccactc	tcttcttcat	tgtccacac	taccatctca	60
tctctccgcc	attttacacc	actcccttct	cgttgcaacc	caacaaattg	gcactgctcg	120
tgcgcgaccc	ctcctccctc	cccgcgtccc	ccgacaagcc	atccgcggcc	atgatcaccg	180
cgtctggacct	ctaccacgtg	ctgacggcgg	tgggtgccgt	gtacgtggcc	atgacgctgg	240
cgtacggctc	cgtccgctgg	tggcgcattc	tcacgcggga	ccagtgtccc	gggatcaacc	300
gcttcgtggc	gctcttcgcc	gtgccgtccc	tctctttcca	cttcatctcc	accaacgacc	360
ccttcgccat	gaacctgcgc	ttcctggccg	ccgacacgct	gcagaagggtg	gccgtcctcg	420
cgtctgtggc	gctggcctcc	cgcggcctct	cctccccgcg	cgcgctcggg	ctcgactgga	480
gcatacagct	cttctccctc	tccacgtccc	ccaacacgct	cgtcatgggc	atcccgtgc	540
tgcgaggcat	gtacggcgcg	tcgtcggccg	gcacgctcat	gggtccaggtc	gtcgtcctcc	600
agtgcattcat	ctggtacacg	ctcatgtctc	tctctttcga	gtaccgcgcc	gcgcgcgcgc	660
tcgtctctga	ccagttcccc	gacggcgccg	ccgcgtccat	cgtctccttc	cgcgtcgact	720
ccgacgtcgt	ctcgtctcgc	aggggggacg	tcgagctcga	ggccgagccc	gacggcgtcg	780
ccggcgccgg	cgcgtctctc	tcccgcggcg	gggacgcggg	gcgggtgcgc	gtcaccgtgc	840
gcaagttccac	cagctcgcgc	tccgaggccg	cgtgctcgca	ctcgcactcc	cagaccatgc	900
agccccgtgt	gtccaacctc	tccggcgtgg	agatctactc	gctgcagtcg	tcgcgcaacc	960
ccaccccgcg	cgggtccagc	ttcaaccacg	ccgacttctt	caacatcgtc	ggcgccgccg	1020
ccaagggagg	cggaggagcg	gcgggggacg	aggagaaggg	gcgatgcggc	ggcggcggcg	1080
gaggacactc	gccgcagccg	caggccgtcg	ccgtgccggc	caagaggaag	gacctgcaca	1140
tgctcgtctg	gagctccagc	gcctcgcccc	tgtccgagcg	cgcgcgcgtg	cacgtcttcg	1200
gcgcccggcg	cgtgaccat	gccgacgtcc	tcgccaaagg	agcccaggcc	tacgacgagt	1260
acggggcgca	cgactacagc	agcaggacga	agaacgggag	cggcggcgcg	gacaagggcg	1320
ggccgacgct	gtcgaagctg	gggtccaact	cgacggcgca	gctgtacccc	aaggacgacg	1380

gcgaggggag	ggcggcggcg	gtggcgatgc	cgccggcgag	cgtagatgacg	cggctcatcc	1440
tcatcatggt	gtggaggaag	ctgatccgga	accccaacac	ctactccage	ctcatcggcg	1500
tcgtctggtc	cctggtctcc	tacaggtggg	gcatcgagat	gccagcgatc	atcgcccggt	1560
cgatttcgat	cctgtcggac	gcgggtctcg	ggatggccat	gttcagccta	ggcctgttca	1620
tggcgctgca	gccgaggatc	atcgcgtagc	ggaacaagct	ggcggccatc	gcgatgggcg	1680
tccggttcgt	cgcaggcccc	gcggtcatgg	ccgccgcctc	catcgccgtc	ggtctgcgcg	1740
gcgtcctcct	ccacatcgcc	atcgccagg	ctgctctgcc	tcaggggatc	gtgccgttcg	1800
tgttcgcaa	ggagtacggc	gttcatcccg	acatcctgag	cacagcgat	ggtccaataa	1860
catcgcatgg	tttcatcact	tgccatagtt	aacgggaaaa	aaaagcagaa	gcaatcgatg	1920
acgagcact	gaattcacta	tgattcatta	ctaattgatg	tgtgttcgat	cagtgcagtc	1980
aaagaaccac	taataagcac	tgatctagga	cagcatcagc	atgattgatt	gcttgttttc	2040
tcctgacaat	ctgcatttct	tactacacag	tgtgccttca	ctcatccatc	cagatgatca	2100
tacaacacta	ctgatgcata	tttttttttg	attctgctgc	agcgtgatct	tcgggatgct	2160
catcgctctg	cccatcacc	tgggtacta	catcttgctg	gggctgtgag	cctctctcgc	2220
tcgttcttc	agcgtgcgga	aggcgccatg	ctgtgggtga	tcggccccac	atgaaatttc	2280
tgatgagcat	tagcgattac	tattagctta	gcgaagaatg	atgagatggt	gtcggcctgt	2340
cgggactggg	ggagtacagc	cagaccccc	tcgaacaaaa	gtttcttttg	gcttctgtcc	2400
gtcagaaaaca	aaagttttgg	cttttggcat	gcgcactcga	agcacagcag	cagcagcagc	2460
atcatccatg	agatgatact	cctctcgaat	cctagagcta	gcgaaggcaa	taataagata	2520
ccacaaggca	atggaatcaa	caaaagcttc	atgcgacgcg	ctatcataatc	aaggaaacaa	2580
tgcagaatac	aacggagtct	agtgcgcaat	ggcttcttct	cttttttttt	cttgcgaaaa	2640
gggtttctag	actgattaaa	ggattccaaa	tagcatctct	ggattcgatt	tctttcgcag	2700
acgaattttc	tggctttttt	agaaaaatcc	tctcgttgaa	aaaaaaaaaa	aaaaaaaaaa	2760
aaaaaaaaag						2760

<210>	14
<211>	573
<212>	PRT
<213>	Zea mays

<400> 14

Met Ile Thr Ala Leu Asp Leu Tyr His Val Leu Thr Ala Val Val Pro
1 5 10 15

Leu Tyr Val Ala Met Thr Leu Ala Tyr Gly Ser Val Arg Trp Trp Arg
20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
50 55 60

Phe Ala Met Asn Leu Arg Phe Leu Ala Ala Asp Thr Leu Gln Lys Val
65 70 75 80

Ala Val Leu Ala Leu Leu Ala Leu Ala Ser Arg Gly Leu Ser Ser Pro
85 90 95

Arg Ala Leu Gly Leu Asp Trp Ser Ile Thr Leu Phe Ser Leu Ser Thr
100 105 110

Leu Pro Asn Thr Leu Val Met Gly Ile Pro Leu Leu Arg Gly Met Tyr
115 120 125

Gly Ala Ser Ser Ala Gly Thr Leu Met Val Gln Val Val Val Leu Gln
130 135 140

Cys Ile Ile Trp Tyr Thr Leu Met Leu Phe Leu Phe Glu Tyr Arg Ala
145 150 155 160

Ala Arg Ala Leu Val Leu Asp Gln Phe Pro Asp Gly Ala Ala Ala Ser
 165 170 175
 Ile Val Ser Phe Arg Val Asp Ser Asp Val Val Ser Leu Ala Arg Gly
 180 185 190
 Asp Val Glu Leu Glu Ala Glu Pro Asp Gly Val Ala Gly Ala Gly Ala
 195 200 205
 Val Ser Ser Arg Gly Gly Asp Ala Gly Arg Val Arg Val Thr Val Arg
 210 215 220
 Lys Ser Thr Ser Ser Arg Ser Glu Ala Ala Cys Ser His Ser His Ser
 225 230 235 240
 Gln Thr Met Gln Pro Arg Val Ser Asn Leu Ser Gly Val Glu Ile Tyr
 245 250 255
 Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe Asn
 260 265 270
 His Ala Asp Phe Phe Asn Ile Val Gly Ala Ala Ala Lys Gly Gly Gly
 275 280 285
 Gly Ala Ala Gly Asp Glu Glu Lys Gly Ala Cys Gly Gly Gly Gly Gly
 290 295 300
 Gly His Ser Pro Gln Pro Gln Ala Val Ala Val Pro Ala Lys Arg Lys
 305 310 315 320
 Asp Leu His Met Leu Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu
 325 330 335
 Arg Ala Ala Val His Val Phe Gly Ala Gly Gly Ala Asp His Ala Asp
 340 345 350
 Val Leu Ala Lys Gly Ala Gln Ala Tyr Asp Glu Tyr Gly Arg Asp Asp
 355 360 365
 Tyr Ser Ser Arg Thr Lys Asn Gly Ser Gly Gly Ala Asp Lys Gly Gly
 370 375 380
 Pro Thr Leu Ser Lys Leu Gly Ser Asn Ser Thr Ala Gln Leu Tyr Pro
 385 390 395 400
 Lys Asp Asp Gly Glu Gly Arg Ala Ala Ala Val Ala Met Pro Pro Ala
 405 410 415
 Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp Arg Lys Leu Ile
 420 425 430
 Arg Asn Pro Asn Thr Tyr Ser Ser Leu Ile Gly Val Val Trp Ser Leu
 435 440 445
 Val Ser Tyr Arg Trp Gly Ile Glu Met Pro Ala Ile Ile Ala Arg Ser
 450 455 460
 Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala Met Phe Ser Leu
 465 470 475 480

```
<220>
<221>  unsure
<222>  (482)
```

<220>
 <221> unsure
 <222> (511)

<220>
 <221> unsure
 <222> (514)

<220>
 <221> unsure
 <222> (519)

<220>
 <221> unsure
 <222> (521)

<220>
 <221> unsure
 <222> (530)

<220>
 <221> unsure
 <222> (535)

<220>
 <221> unsure
 <222> (543)

<400> 15
 gagcgacgtc gagatgaacg gcgccgtcgt cgcgggcgccg gngcgggcggc ggcggcggtcc 60
 ggctaccgtt ctggggcgacg gcgaggacgg tggggctgaa gctggcgagg aacccgaacg 120
 tgtacgccag cgttctcggc gtcgtgtggg cgtgcatcgc gtacaggtgg cacctgagct 180
 tgccggggat cgtgacgggg tcgctgcagg tgatgtccag gactggcacg gggatgtcca 240
 tgttcagcat ggggttggtc atggggcagc aggagagggt gatagcgtgc ggggcggggc 300
 tgacggcgct ggggatggcg ctgcgggttcg tcgccgggtcc gtcgcccacg ctcgtcgggc 360
 ccgcgcacct cggncctccgc ggcgacgtcc tgcacctcgc catcatacag gncgnactgc 420
 tcaatcgatt nttcttcgtt ttncaaagga gtatggctta ttncgatgac tcagnacggc 480
 gntatattcg gacattatcc tgtgcgatct nttnaatang ngggttgggg ttgtnaaatc 540
 atn 543

<210> 16
 <211> 110
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (108)..(109)

<400> 16
 Val Gly Leu Lys Leu Ala Arg Asn Pro Asn Val Tyr Ala Ser Val Leu
 1 5 10 15
 Gly Val Val Trp Ala Cys Ile Ala Tyr Arg Trp His Leu Ser Leu Pro
 20 25 30
 Gly Ile Val Thr Gly Ser Leu Gln Val Met Ser Arg Thr Gly Thr Gly
 35 40 45

Met Ser Met Phe Ser Met Gly Leu Phe Met Gly Gln Gln Glu Arg Val
 50 55 60

Ile Ala Cys Gly Ala Gly Leu Thr Ala Leu Gly Met Ala Leu Arg Phe
 65 70 75 80

Val Ala Gly Pro Leu Ala Thr Leu Val Gly Ala Ala Ala Leu Gly Leu
 85 90 95

Arg Gly Asp Val Leu His Leu Ala Ile Ile Gln Xaa Xaa Leu
 100 105 110

<210> 17
 <211> 330
 <212> DNA
 <213> Oryza sativa

<400> 17
 ctccactcgg ccgctcctgc atgtataact agctagttct agctcgctca ggcactcgat 60
 ccaccgccgg gcgcgttgga ttgagatagg ctgaggagat gatatccggg cactgacttct 120
 acacggtgat ggcggcgggtg gtgccgctgt acgtggcgat gttcctggcg tacgggtcgg 180
 tgcggtggtg gggcatcttc acgccggacc agtgctccgg catcaaccgc ttcgtcgcca 240
 tcttcgccgt gccgtcctg tccttccact tcattctccac caacgaccgg tacgccatga 300
 acctccgctt cctggcggcg ggacacgctg 330

<210> 18
 <211> 74
 <212> PRT
 <213> Oryza sativa

<400> 18
 Met Ile Ser Gly His Asp Phe Tyr Thr Val Met Ala Ala Val Val Pro
 1 5 10 15

Leu Tyr Val Ala Met Phe Leu Ala Tyr Gly Ser Val Arg Trp Trp Gly
 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Ile
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
 50 55 60

Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala
 65 70

<210> 19
 <211> 2162
 <212> DNA
 <213> Oryza sativa

<400> 19
 ctccactcgg ccgctcctgc atgtataact agctagttct agctcgctca ggcactcgat 60
 ccaccgccgg gcgcgttgga ttgagatagg ctgaggagat gatatccggg cactgacttct 120
 acacggtgat ggcggcgggtg gtgccgctgt acgtggcgat gttcctggcg tacgggtcgg 180
 tgcggtggtg gggcatcttc acgccggacc agtgctccgg catcaaccgc ttcgtcgcca 240
 tcttcgccgt gccgtcctg tccttccact tcattctccac caacgaccgg tacgccatga 300
 acctccgctt cctggcggcg gacacgctgc agaagctgct cgtcctggcg ggcctcgccg 360
 cgtggtcgcg cctcccctcg cggaccggcg cgccgaggct ggactggtcc atcacgctct 420
 tctccctctc cactgctgcc aacacgctcg tcattgggat cccgctgctg atcgccatgt 480


```

acggggccata ctccggctcg ctcatggtcc agatcgctcg gctccagtgc atcatctggt 540
acacgctgat gctcttcttc ttcgagttcc ggcgcgcgcg gatgctgac gccgaccagt 600
tcccggacac ggcggcgtcc atcgtgtccc tgcacgtcga cccggacgtg gtgtcgctgg 660
agggcgccca cgcggagacg gaggccgagg tggcggcgga cgggcggctg cacgtcaccg 720
tgcgccggtc ctccggtgctg cggcggtcgc tgctggtcac gccgcggccg tcgaacctga 780
cgggagcgga gatctactcg cttagctcgt cgcggaaccc aaccccgcgg ggctccaact 840
tcaaccacgc cgacttcttc gccatggtcg ggcgcgggcc accgcccccg acgcccgtg 900
cgggtgcgcg ctcgagcttc ggcgcctccg agctttactc gctgcaatcg tcgcggggcc 960
caaccccgag gcagtcacaac ttcgacgagc actcggcacg gccgcgaaa ccaccggcaa 1020
cgaccacggg ggcaactcaac cacgatgcca aggagctcca catgttcgtg tggagctcga 1080
gcgcgtctcc cgtctcagaa gtcagcggcc tgctgtgtt cagtggcggc ggcgcgcgcg 1140
gcgctctcga cgtcggcgcc aaggaaatcc acatggtcat ccccgccgac ctgccgcaga 1200
acaacggctc aggcaaagag cagcaggagt acggcgcagt ggcattgggt ggcgcgcgcg 1260
gcggagagaa cttcagcttc ggaggcgga agacggtgga cggcgccgag gcagtagacg 1320
aggaggcggc cttgcctgac gggctgacga agatggggtc gagctcgac gcggagctgc 1380
acccgaaggt cgtcgacgtc gacggaccga acgcggcgcg cggcgcccgg ggcgcggggc 1440
agtaccaaat gccgcggcg agcgtgatga cacgcctcat cctcataatg gtgtggcgca 1500
agctcatccg caaccccaac acttactcca gcctcctcgg cctcgcttg tccctcgctg 1560
ccttcgggat tgttcattggc gctgcagccc agcatcatcg cgtgtggcaa atcagccgac 1620
gtcgtctcca tggcgtccg cttcctcgcg ggcctgccc tcattggccg cgcgtcaatc 1680
gccatcgga cccgcgggac gctcctgcac gtcgccattg ttcaggcggc tctaccacaa 1740
gggattgtgc cttttgttt tgcaaaagaa tacaatgtcc acccggccat cctgagcaca 1800
gcggtaat tttggcatgct aatagctctt ccaatcacat tgctgtacta catccttctt 1860
ggactatgat caagaaagct tatggacgt ctcacataaa acggaagaaa tgggggcaaa 1920
gagagagaaa aaaaagcgat cctgtccatc tcaaacagcg tatgcttata tgtatagcct 1980
gttgtcggac attgcccattg atgacaagac aacgaagttg ttacagagct atatatctct 2040
gcgacatttg tacaagagat aacgacagaa tgtactcaaa tataaccgat attagatatg 2100
tggtctgtta aagatctcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2160
aa 2162

```

<210> 20
 <211> 589
 <212> PRT
 <213> *Oryza sativa*

<400> 20
 Met Ile Ser Gly His Asp Phe Tyr Thr Val Met Ala Ala Val Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Phe Leu Ala Tyr Gly Ser Val Arg Trp Trp Gly
 20 25 30
 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Ile
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
 50 55 60
 Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala Asp Thr Leu Gln Lys Leu
 65 70 75 80
 Leu Val Leu Ala Gly Leu Ala Ala Trp Ser Arg Leu Pro Ser Arg Thr
 85 90 95
 Gly Ala Pro Arg Leu Asp Trp Ser Ile Thr Leu Phe Ser Leu Ser Thr
 100 105 110
 Leu Pro Asn Thr Leu Val Met Gly Ile Pro Leu Leu Ile Ala Met Tyr
 115 120 125

WO 00/68389

PCT/US00/12061

Gly	Pro	Tyr	Ser	Gly	Ser	Leu	Met	Val	Gln	Ile	Val	Val	Leu	Gln	Cys
130						135					140				
Ile	Ile	Trp	Tyr	Thr	Leu	Met	Leu	Phe	Leu	Phe	Glu	Phe	Arg	Ala	Ala
145					150					155					160
Arg	Met	Leu	Ile	Ala	Asp	Gln	Phe	Pro	Asp	Thr	Ala	Ala	Ser	Ile	Val
				165					170					175	
Ser	Leu	His	Val	Asp	Pro	Asp	Val	Val	Ser	Leu	Glu	Gly	Gly	His	Ala
			180					185					190		
Glu	Thr	Glu	Ala	Glu	Val	Ala	Ala	Asp	Gly	Arg	Leu	His	Val	Thr	Val
		195					200					205			
Arg	Arg	Ser	Ser	Val	Ser	Arg	Arg	Ser	Leu	Leu	Val	Thr	Pro	Arg	Pro
	210					215					220				
Ser	Asn	Leu	Thr	Gly	Ala	Glu	Ile	Tyr	Ser	Leu	Ser	Ser	Ser	Arg	Asn
225					230					235					240
Pro	Thr	Pro	Arg	Gly	Ser	Asn	Phe	Asn	His	Ala	Asp	Phe	Phe	Ala	Met
				245					250					255	
Val	Gly	Gly	Gly	Pro	Pro	Pro	Pro	Thr	Pro	Ala	Ala	Val	Arg	Gly	Ser
			260					265					270		
Ser	Phe	Gly	Ala	Ser	Glu	Leu	Tyr	Ser	Leu	Gln	Ser	Ser	Arg	Gly	Pro
		275					280					285			
Thr	Pro	Arg	Gln	Ser	Asn	Phe	Asp	Glu	His	Ser	Ala	Arg	Pro	Pro	Lys
	290					295					300				
Pro	Pro	Ala	Thr	Thr	Thr	Gly	Ala	Leu	Asn	His	Asp	Ala	Lys	Glu	Leu
305					310					315					320
His	Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	Ser	Glu	Val	Ser
				325					330					335	
Gly	Leu	Pro	Val	Phe	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Leu	Asp	Val
		340						345					350		
Gly	Ala	Lys	Glu	Ile	His	Met	Val	Ile	Pro	Ala	Asp	Leu	Pro	Gln	Asn
		355					360					365			
Asn	Gly	Ser	Gly	Lys	Glu	His	Glu	Glu	Tyr	Gly	Ala	Val	Ala	Leu	Gly
	370					375					380				
Gly	Gly	Gly	Gly	Gly	Glu	Asn	Phe	Ser	Phe	Gly	Gly	Gly	Lys	Thr	Val
385					390					395					400
Asp	Gly	Ala	Glu	Ala	Val	Asp	Glu	Glu	Ala	Ala	Leu	Pro	Asp	Gly	Leu
				405					410					415	
Thr	Lys	Met	Gly	Ser	Ser	Ser	Thr	Ala	Glu	Leu	His	Pro	Lys	Val	Val
			420					425					430		
Asp	Val	Asp	Gly	Pro	Asn	Ala	Gly	Gly	Gly	Ala	Ala	Gly	Ala	Gly	Gln
		435					440							445	

Tyr Gln Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met
 450 455 460
 Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Leu
 465 470 475 480
 Gly Leu Ala Trp Ser Leu Val Ala Phe Arg Leu Phe Met Ala Leu Gln
 485 490 495
 Pro Ser Ile Ile Ala Cys Gly Lys Ser Ala Ala Val Val Ser Met Ala
 500 505 510
 Val Arg Phe Leu Ala Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala
 515 520 525
 Ile Gly Leu Arg Gly Thr Leu Leu His Val Ala Ile Val Gln Ala Ala
 530 535 540
 Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val
 545 550 555 560
 His Pro Ala Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala
 565 570 575
 Leu Pro Ile Thr Leu Leu Tyr Tyr Ile Leu Leu Gly Leu
 580 585

<210> 21
 <211> 1618
 <212> DNA
 <213> Glycine max

<400> 21
 gcacgaggat ctctgagcag ttcccagaca ctgccggtac cattgtctcc atccatgtcg 60
 actctgatgt catgtctctt gacggacgac agcaccctct ggaaaccgat gcccaaataca 120
 aagaggacgg caagctccac gtcactgtca gaaaatccaa cgcttccaga tccgacatct 180
 tttctagaag gtcccagggc ttctcttcca ccaccctctg cccttccaat ctcaccaatg 240
 ctgagattta ctctcttcag tcctctcgaa accctactcc acgtggctcc agtttcaacc 300
 acaccgattt ctactccatg atggctgctg gtcgtaattc taactttggt gccaacgatg 360
 tttatggcct ttctgcttcc agaggaccaa ctcccagacc ttccaattac gacgaggatg 420
 cttctaataa taacaatggg aagccgaggt accactaccc tgctgctgga acaggaacag 480
 gaacaggaac aggaacggga acgggaacag ggcactaccc tgctcctaac cctggcatgt 540
 tctctcccac tgcttctaaa aacgtcgcca agaagccaga cgatccaaat aaggaccttc 600
 atatgttctg ttggagttca agtgcttccc cggtttcgga tgtgtttggt ggtggacatg 660
 aatatgatca taaagaactc aagttaactg tatctccagg aaaagtggag ggtaatatca 720
 atagagacac tcaagaggag taccagccag agaaagatga atttagtttt ggaaacagag 780
 ggattgagga tgagcatgaa ggtgagaaag ttggaaacgg aaatccaaaa acaatgcctc 840
 cagcaagtgt aatgacgagg ctatttttga tcatggtgtg gaggaaactt atcagaaacc 900
 ccaacacctt ctccagccta atcggcctaa cttggtcact catttcattc aggtggaacg 960
 taaaaatgcc agccataatt gccaaagtcta tttcgatatt gtcagatgca gggcttggga 1020
 tggccatgtt tagtcttggg ctgttcattg ctttgcaacc gaggatcata gcatgtggaa 1080
 attccacagc agctttttct atggccgtga gattccttac aggtccagct gtcattggcag 1140
 ctgcttccat tgctgttgga ctcaaaggcg ttctcttgca cgttgctatt gttcaggcag 1200
 ctcttctctc aggaattgtc ccatttgtct ttgccaagga atacaatgta catcctgata 1260
 ttctcagtac ggggtgttatt tttgggatgt tgattgcatt gccattacg ctctgtgtact 1320
 acatcttgct ggggttatga gtgaatgaga agatggagga tatgaagatt acatgtggca 1380
 tggcatgcat gcaatctcgt ttgagactcc ttagagcacg acaacaaatg ttcaatgaaa 1440
 tacaaaagca tcaccataat tgaataggag gaatcgatca acggatgagt ttctattttt 1500
 cttcttcttt tttttttaat gaattgtcct tgctcagtga aaatgtaaaa tcatgtttgt 1560
 agctaattta taaaatggct atctcgtaa atttcaaatt aaaaaaaaaa aaaaaaaa 1618

<210> 22
 <211> 443
 <212> PRT
 <213> Glycine max

<400> 22

```

Ile Ser Glu Gln Phe Pro Asp Thr Ala Gly Thr Ile Val Ser Ile His
 1              5              10              15

Val Asp Ser Asp Val Met Ser Leu Asp Gly Arg Gln His Pro Leu Glu
          20              25              30

Thr Asp Ala Gln Ile Lys Glu Asp Gly Lys Leu His Val Thr Val Arg
          35              40              45

Lys Ser Asn Ala Ser Arg Ser Asp Ile Phe Ser Arg Arg Ser Gln Gly
          50              55              60

Phe Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile
 65              70              75              80

Tyr Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe
          85              90              95

Asn His Thr Asp Phe Tyr Ser Met Met Ala Ala Gly Arg Asn Ser Asn
          100              105              110

Phe Gly Ala Asn Asp Val Tyr Gly Leu Ser Ala Ser Arg Gly Pro Thr
          115              120              125

Pro Arg Pro Ser Asn Tyr Asp Glu Asp Ala Ser Asn Asn Asn Asn Gly
          130              135              140

Lys Pro Arg Tyr His Tyr Pro Ala Ala Gly Thr Gly Thr Gly Thr Gly
          145              150              155              160

Thr Gly Thr Gly Thr Gly Thr Gly His Tyr Pro Ala Pro Asn Pro Gly
          165              170              175

Met Phe Ser Pro Thr Ala Ser Lys Asn Val Ala Lys Lys Pro Asp Asp
          180              185              190

Pro Asn Lys Asp Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro
          195              200              205

Val Ser Asp Val Phe Gly Gly Gly His Glu Tyr Asp His Lys Glu Leu
          210              215              220

Lys Leu Thr Val Ser Pro Gly Lys Val Glu Gly Asn Ile Asn Arg Asp
          225              230              235              240

Thr Gln Glu Glu Tyr Gln Pro Glu Lys Asp Glu Phe Ser Phe Gly Asn
          245              250              255

Arg Gly Ile Glu Asp Glu His Glu Gly Glu Lys Val Gly Asn Gly Asn
          260              265              270

Pro Lys Thr Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile
          275              280              285

```

Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu
 290 295 300

Ile Gly Leu Thr Trp Ser Leu Ile Ser Phe Arg Trp Asn Val Lys Met
 305 310 315 320

Pro Ala Ile Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu
 325 330 335

Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Arg
 340 345 350

Ile Ile Ala Cys Gly Asn Ser Thr Ala Ala Phe Ser Met Ala Val Arg
 355 360 365

Phe Leu Thr Gly Pro Ala Val Met Ala Ala Ala Ser Ile Ala Val Gly
 370 375 380

Leu Lys Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro
 385 390 395 400

Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro
 405 410 415

Asp Ile Leu Ser Thr Gly Val Ile Phe Gly Met Leu Ile Ala Leu Pro
 420 425 430

Ile Thr Leu Val Tyr Tyr Ile Leu Leu Gly Leu
 435 440

<210> 23
 <211> 531
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (530)

<400> 23
 tctgacactc cctcacttca tccttctaca cattcacatc ttctctgaaa caattacaaa 60
 gtgagtgtgaaa gtagtgtcct agcactagta gtacagtaca gaaaactaga agagcaacca 120
 aaattttcca attagcacta gtagtacagt acaaaaaact agaagagcaa ccaaaatttt 180
 ccaattgaaa aagaaataac aacgagaaca aaatcttattc gtgagatcga ataactgaaa 240
 aaaaaggaaa gaagaacaaa aaatgataac gtggaaagac ctatacacgg tcctgaccgc 300
 agtgggtccct ctctacgtgg cgatgatcct ggcgtacggc tcggtccggt ggtggaaaga 360
 tcttctcacc ggaccagtgc tccggcataa accgcttcgt ggcgatcttc gccgtgccgc 420
 tcctctcctt ccacttcac tccaccaaca acccctacgc catgaacttc cgcttcaccc 480
 gccgccggac acctccaaga agatcatcat gctcttcgcc cttgcaaccn g 531

<210> 24
 <211> 90
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (33)

<220>

<221> UNSURE

<222> (78)

<400> 24

Met Ile Thr Trp Lys Asp Leu Tyr Thr Val Leu Thr Ala Val Val Pro
 1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Lys
 20 25 30

Xaa Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala
 35 40 45

Ile Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn
 50 55 60

Pro Tyr Ala Met Asn Phe Arg Phe Ile Arg Arg Arg Thr Xaa Thr Ser
 65 70 75 80

Lys Lys Ile Ile Met Leu Phe Ala Leu Ala
 85 90

<210> 25

<211> 2101

<212> DNA

<213> Glycine max

<400> 25

ctttctctga	cactccctca	cttcctcctt	ctacacattc	acatcttctc	tgaacaatt	60
acaaagttag	tgaagttagt	gtcctagcac	tagtagtaca	gtacagaaaa	ctagaagagc	120
aacaaaaatt	ttccaattag	cactagtagt	acagtacaaa	aaactagaag	agcaacaaaa	180
attttccaat	tgaaaaaagaa	ataacaacga	gaacaaaatc	ttatcgtgag	atcgaataac	240
tgaaaaaaaaa	ggaaagaaga	acaaaaaatg	ataacgtgga	aagacctata	cacggtcctg	300
accgcagtgg	tccctctcta	cgtggcgatg	atcctggcgt	acggctcggg	ccgggtgggtg	360
aagatcttct	caccggacca	gtgctccggc	ataaacccgt	tcgtggcgat	cttcgccgtg	420
ccgctcctct	ccctccactt	catctccacc	aacaaccctt	acgccatgaa	cttcgcgttc	480
atcgccgcgc	acaccctcca	gaagatcatc	atgctcttcg	cccttgccat	ctggaccaac	540
ctcacaaaaa	ccggttccct	agagtggatg	attaccatct	tctccctctc	aacccttccc	600
aataccttag	tcatgggaat	tccactccta	atcgccatgt	acggcgacta	ctccggctcg	660
ctcatgggtc	aggctcgtgt	ccttcagtgc	atcatatggt	acaccttggt	gctcttctta	720
ttcgaatacc	gcgccgcgaa	aatcctaate	atggaacagt	tccttgaaac	cgctgcctcc	780
atcgtgtcgt	ttaaagtcga	ctccgacgtc	gtttcgctcg	acgggagggg	cttcttgagg	840
accgacgcgc	aagtcggtga	cgatgggaag	cttcattgtc	ccgttagaaa	gtcgaacgcc	900
tcgcgtaggt	cgtttatgat	gacgccgagg	ccttctaate	tactggggc	ggagatttac	960
agcctcagct	cgtctcgtaa	cccaacacca	cgtggctcaa	actttaacca	tgcggttttc	1020
ttctccatga	tggggtacca	gcctcgccac	tccaatttca	cggccaatga	tttgttctcc	1080
tcgcgtggac	ccactccgag	gccttctaate	ttcgaagaac	cctcaatgcc	tcaggcggtg	1140
acggtagctt	ctcctcggtt	cgggttctac	ccgtcccaaa	ccgtgccagc	ttcgtaccgc	1200
ccgcccaccc	cggatttttc	ctccgctact	aaaaacttga	agaatcaaag	tcagaatcag	1260
aatccgaacc	agagccagag	ccagaattcg	caggctccgg	cgaagggtgc	ccacgatgcg	1320
aaggagctcc	acatgtttgt	gtggagctcc	agtgcctccc	cgatgtcgga	gaatgccgga	1380
ctcaacgtct	ttagcagcac	agacctcgga	acctccgaac	aacctgacca	gggtgctaaa	1440
gagattagga	tgttggtggc	tgataataat	gcacacttac	gaaatggtga	agccaacaac	1500
aaaggtggtt	tggaggcagt	acttggtgtg	gaagacttca	agtttctggt	gaatggcgaa	1560
gaacaagtgt	gggaagaaaa	agaagggtcg	aacaatgggc	ttaacaagtt	gggtcaagc	1620
tccacggttg	agctccaacc	aaaagccacc	gtagccggcg	aggcttccgc	cggaaaacac	1680
atgcctccgg	caaagtcat	gactcgtctc	atactcatca	tgggtgtggg	aaagcttatc	1740
cgcaatccca	acacatactc	tagcctaatt	ggtgtagtat	ggctccctcg	tgcatcagc	1800
tggcacgtgc	atatgcccac	aataatagag	aatcaattt	ccatactgtc	tgatgccggt	1860

cttggaatgg ctatgttcag cttaggtgac tggtcgcaaa tccattctcc aaattcatatc 1920
 tctcgcgaaa taatttcatt cttttatcca aaaacaattt cgcttccttc ttccccatag 1980
 atcattatctt tattggctcc aattgttagt gtaaagtgtg atttccttat actaagaaaa 2040
 taaaatgcat gtgtttaatt atctatttat ttatttctga cccaaaaaaa aaaaaaaaaa 2100
 a 2101

<210> 26
 <211> 540
 <212> PRT
 <213> Glycine max

<400> 26

Met	Ile	Thr	Trp	Lys	Asp	Leu	Tyr	Thr	Val	Leu	Thr	Ala	Val	Val	Pro
1				5					10					15	
Leu	Tyr	Val	Ala	Met	Ile	Leu	Ala	Tyr	Gly	Ser	Val	Arg	Trp	Trp	Lys
			20					25					30		
Ile	Phe	Ser	Pro	Asp	Gln	Cys	Ser	Gly	Ile	Asn	Arg	Phe	Val	Ala	Ile
		35					40					45			
Phe	Ala	Val	Pro	Leu	Leu	Ser	Phe	His	Phe	Ile	Ser	Thr	Asn	Asn	Pro
	50					55					60				
Tyr	Ala	Met	Asn	Phe	Arg	Phe	Ile	Ala	Ala	Asp	Thr	Leu	Gln	Lys	Ile
65					70					75					80
Ile	Met	Leu	Phe	Ala	Leu	Ala	Ile	Trp	Thr	Asn	Leu	Thr	Lys	Thr	Gly
				85					90					95	
Ser	Leu	Glu	Trp	Met	Ile	Thr	Ile	Phe	Ser	Leu	Ser	Thr	Leu	Pro	Asn
			100					105					110		
Thr	Leu	Val	Met	Gly	Ile	Pro	Leu	Leu	Ile	Ala	Met	Tyr	Gly	Asp	Tyr
		115					120					125			
Ser	Gly	Ser	Leu	Met	Val	Gln	Val	Val	Val	Leu	Gln	Cys	Ile	Ile	Trp
	130					135					140				
Tyr	Thr	Leu	Leu	Leu	Phe	Leu	Phe	Glu	Tyr	Arg	Ala	Ala	Lys	Ile	Leu
145					150					155					160
Ile	Met	Glu	Gln	Phe	Pro	Glu	Thr	Ala	Ala	Ser	Ile	Val	Ser	Phe	Lys
				165					170					175	
Val	Asp	Ser	Asp	Val	Val	Ser	Leu	Asp	Gly	Arg	Asp	Phe	Leu	Glu	Thr
			180					185					190		
Asp	Ala	Glu	Val	Gly	Asp	Asp	Gly	Lys	Leu	His	Val	Thr	Val	Arg	Lys
		195					200					205			
Ser	Asn	Ala	Ser	Arg	Arg	Ser	Phe	Met	Met	Thr	Pro	Arg	Pro	Ser	Asn
	210					215					220				
Leu	Thr	Gly	Ala	Glu	Ile	Tyr	Ser	Leu	Ser	Ser	Ser	Arg	Asn	Pro	Thr
225					230					235				240	
Pro	Arg	Gly	Ser	Asn	Phe	Asn	His	Ala	Asp	Phe	Phe	Ser	Met	Met	Gly
				245					250					255	

Tyr Gln Pro Arg His Ser Asn Phe Thr Ala Asn Asp Leu Phe Ser Ser
 260 265 270
 Arg Gly Pro Thr Pro Arg Pro Ser Asn Phe Glu Glu Pro Ser Met Pro
 275 280 285
 Gln Ala Val Thr Val Ala Ser Pro Arg Phe Gly Phe Tyr Pro Ser Gln
 290 295 300
 Thr Val Pro Ala Ser Tyr Pro Pro Pro Asn Pro Asp Phe Ser Ser Ala
 305 310 315 320
 Thr Lys Asn Leu Lys Asn Gln Ser Gln Asn Gln Asn Pro Asn Gln Ser
 325 330 335
 Gln Ser Gln Asn Ser Gln Ala Pro Ala Lys Gly Ala His Asp Ala Lys
 340 345 350
 Glu Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Met Ser Glu
 355 360 365
 Asn Ala Gly Leu Asn Val Phe Ser Ser Thr Asp Leu Gly Thr Ser Glu
 370 375 380
 Gln Pro Asp Gln Gly Ala Lys Glu Ile Arg Met Leu Val Ala Asp Asn
 385 390 395 400
 Asn Ala His Leu Arg Asn Gly Glu Ala Asn Asn Lys Gly Gly Leu Glu
 405 410 415
 Ala Val Leu Gly Val Glu Asp Phe Lys Phe Leu Val Asn Gly Glu Glu
 420 425 430
 Gln Val Gly Glu Glu Lys Glu Gly Leu Asn Asn Gly Leu Asn Lys Leu
 435 440 445
 Gly Ser Ser Ser Thr Val Glu Leu Gln Pro Lys Ala Thr Val Ala Gly
 450 455 460
 Glu Ala Ser Ala Gly Lys His Met Pro Pro Ala Asn Val Met Thr Arg
 465 470 475 480
 Leu Ile Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr
 485 490 495
 Tyr Ser Ser Leu Ile Gly Val Val Trp Ser Leu Val Ala Phe Arg Trp
 500 505 510
 His Val His Met Pro Lys Ile Ile Glu Lys Ser Ile Ser Ile Leu Ser
 515 520 525
 Asp Ala Gly Leu Gly Met Ala Met Phe Ser Leu Gly
 530 535 540

<210> 27
 <211> 525
 <212> DNA
 <213> Glycine max

<400> 27
 cccactctgt ccttgtgctt tggagactgc aagtgcaccc ttgcttgagc ctctcaaagc 60
 tgaaaaaata tttgctgtat tctctgctgc acattagcac cattcactca ctccactgcc 120
 caaaaccaca tgctcttcca catccctata taaaatcttt tcaatcttca taatcatcat 180
 catcaccacc aactccaact caaactctcc aaaacctgcc acttcaacct tcctatatat 240
 tccttccttc actctcttct gcttctatca tctttctgag aggcttggtg acacacaaaa 300
 aatgatcacc ttaacagact tctaccatgt gatgactgca atggtgccac tctatgtggc 360
 catgatacta gcctatggct cagtgaagtgt gtggaagatt ttctcccctg ataatgctct 420
 ggcatacaacc gttttgtggc actctttgca gtgcctcttc tctcctttca cttcatagcc 480
 tcaaacaacc ctttatgaga tgaacctgaa ggtcctaact ggctg 525

<210> 28
 <211> 64
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (38)

<400> 28
 Met Ile Thr Leu Thr Asp Phe Tyr His Val Met Thr Ala Met Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Lys
 20 25 30
 Ile Phe Ser Pro Asp Xaa Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ser Asn Asn Pro
 50 55 60

<210> 29
 <211> 2549
 <212> DNA
 <213> Glycine max

<400> 29
 gcacgagccc cactctgcct tgtgctttgg agactgcaag tgcaaccttg cttgcagctc 60
 tcaaagctga aaaaatattt gctgtattct ctgctgcaca ttagcaccat tcactcactc 120
 actgcccaca aaccacatgc tcttccacat cctatatata aatcttttca atcttcataa 180
 tcatcatcat caccaccaac tccaactcaa actctccaaa acctgccact tcaaccttcc 240
 tatatatattc ttccctcact ctcttctgct tctatcatct ttctgagagg cttgttgaca 300
 cacaaaaaat gatcacctta acagacttct accatgtgat gactgcaatg gtgccactct 360
 atgtggccat gatactagcc tatggctcag tgaagtgggt gaagattttc tcccctgatc 420
 aatgctctgg catcaaccgt tttgtggcac tctttgcagt gcctcttctc tccttccact 480
 tcatagcctc caacaaccct tatgagatga acctgaggtt cctagctgct gacacccttc 540
 aaaagatcat aatactagtc ctcttgcag tttggagcaa catcaccaaa aggggttggt 600
 tggaatgggc cataaccttg ttctctctct ccacctccc aaacactttg gttatgggca 660
 tccctttgct caaagggatg tatggtgact tctcagggag cctcatggtg caaattgtgg 720
 tcctccagtg catcatttgg tacaccttga tgccttctt gtttgagttt agaggtgcca 780
 gaatgctcat ctctgagcag ttccctgaca ctgctgcctc cattgtctcc atccatgtgg 840
 actctgatgt catgtcattg gatggaagac aaccttga gactgaagct gagatcaagg 900
 aagatggtaa actccatgtc actgtgagga aatccaatgc ttcaagatca gacatcttct 960
 ctagaaggtc tcaggggtctc tcttccacca ctccacgcc ttccaacctt accaatgctg 1020
 agatatactc tttgcaatcc tctaggaacc ctacgccgag aggctctagt ttcaaccaca 1080
 ctgatttcta ctccatgatg gctgctgggt gcaggaactc aaactttggt gcctctgatg 1140
 tttatggcct tttagcttca agagggccaa ctccaaggcc ttctaactat gatgaagatg 1200
 gtgggaagcc aaagtttcat taccatgctg ctggtggaac tgggcactac cctgcaccaa 1260

<210>	30
<211>	605
<212>	PRT
<213>	Glycine max

Met Ile Thr Leu Thr Asp Phe Tyr His Val Met Thr Ala Met Val Pro
1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Lys
20 25 30

Ile Phe Ser Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ser Asn Asn Pro
50 55 60

Tyr Glu Met Asn Leu Arg Phe Leu Ala Ala Asp Thr Leu Gln Lys Ile
65 70 75 80

Ile Ile Leu Val Leu Leu Ala Val Trp Ser Asn Ile Thr Lys Arg Gly
85 90 95

Cys Leu Glu Trp Ala Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
100 105 110

Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asp Phe
115 120 125

Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp
130 135 140

Tyr Thr Leu Met Leu Phe Leu Phe Glu Phe Arg Gly Ala Arg Met Leu
145 150 155 160

Ile Ser Glu Gln Phe Pro Asp Thr Ala Ala Ser Ile Val Ser Ile His
 165 170 175
 Val Asp Ser Asp Val Met Ser Leu Asp Gly Arg Gln Pro Leu Glu Thr
 180 185 190
 Glu Ala Glu Ile Lys Glu Asp Gly Lys Leu His Val Thr Val Arg Lys
 195 200 205
 Ser Asn Ala Ser Arg Ser Asp Ile Phe Ser Arg Arg Ser Gln Gly Leu
 210 215 220
 Ser Ser Thr Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile Tyr
 225 230 235 240
 Ser Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe Asn
 245 250 255
 His Thr Asp Phe Tyr Ser Met Met Ala Ala Gly Gly Arg Asn Ser Asn
 260 265 270
 Phe Gly Ala Ser Asp Val Tyr Gly Leu Ser Ala Ser Arg Gly Pro Thr
 275 280 285
 Pro Arg Pro Ser Asn Tyr Asp Glu Asp Gly Gly Lys Pro Lys Phe His
 290 295 300
 Tyr His Ala Ala Gly Gly Thr Gly His Tyr Pro Ala Pro Asn Pro Gly
 305 310 315 320
 Met Phe Ser Pro Ser Asn Gly Ser Lys Ser Val Ala Ala Asn Ala Asn
 325 330 335
 Ala Lys Arg Pro Asn Gly Gln Ala Gln Leu Lys Pro Glu Asp Gly Asn
 340 345 350
 Arg Asp Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser
 355 360 365
 Asp Val Phe Gly Ala His Glu Tyr Gly Gly Gly His Asp Gln Lys Glu
 370 375 380
 Val Lys Leu Asn Val Ser Pro Gly Lys Val Glu Asn Asn His Arg Asp
 385 390 395 400
 Thr Gln Glu Asp Tyr Leu Glu Lys Asp Glu Phe Ser Phe Gly Asn Arg
 405 410 415
 Glu Met Asp Arg Glu Met Asn Gln Leu Glu Gly Glu Lys Val Gly Asp
 420 425 430
 Gly Lys Pro Lys Thr Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile
 435 440 445
 Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser
 450 455 460
 Ser Leu Ile Gly Leu Thr Trp Ser Leu Val Ser Phe Lys Trp Asn Val
 465 470 475 480

<220>
<221> UNSURE
<222> (25)

<220>
 <221> UNSURE
 <222> (32)

<220>
 <221> UNSURE
 <222> (64)

<400> 32

Met Ile Thr Gly Lys Asp Ile Tyr Asp Val Phe Ala Ala Ile Val Pro
 1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ser Xaa Tyr Gly Ser Val Arg Trp Xaa
 20 25 30

Lys Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala
 35 40 45

Val Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Xaa
 50 55 60

Pro Tyr Ala Met Asn Tyr His Phe Ile Ala Ala Asp Cys Leu Gln Lys
 65 70 75 80

Val Val Ile Leu

<210> 33
 <211> 2324
 <212> DNA
 <213> Glycine max

<400> 33

```
gcacgagctt tatcgtgaga gttttgcctt tattttctcag ccatgtttcc ttcttttcca 60
gcttaaaccg ctaccctaca aaacctttca caatttctctt tcttcctagc tatctctttc 120
tttctgtcta cattgacctt gctagctaca aacctgtcat taacctgat cactggtaag 180
gatatttatg atgttttcgc ggctattgtg cccctctacg ttgctatgat attagcatac 240
ggctcagttc ggtggtggaa aattttcaca cctgatcaat gttctggcat aaaccgcttc 300
gttgctgtgt tcgcagttcc acttctttct ttccacttca tctcctccaa tgacccttat 360
gctatgaact accacttcat agcagctgat tgtcttcaaa aagttgtcat tttgggtgct 420
ctctttctat ggaacacctt cacaaaacat ggtagcctag actggacaat caccctcttc 480
tcactttcaa ccttccaaa cacacttgct atggggatcc ctctattgaa ggccatgtat 540
ggagacttct cagggagcct catggtccaa attgtggtgt tgcaaagtgt gatatgggat 600
accctcatgc tgttcatgtt tgaatataga ggtgcaaaac tctcatcac agaacagttc 660
cctgagactg caggctccat aacttccttc aggggtgact cagatgttgt ctcaactcaat 720
ggtagagagc cacttcaaac agatgctgag ataggagaag atggaaaact tcatgtggtt 780
gttaaaagat cagcagcttc ttccatgata tcttcattca acaagtctca ttttaacttc 840
atgacaccaa gagcatctaa cctcactggg gttgagatct attctgttca gtcatacaaga 900
gaaccaaccc caagaggttc gagtttcaac caaacggatt tctatgccat gttcgcaagc 960
aaggcaccga gtccaaaaca tggctacaca aacagtttcc agagtaataa tgggtggtatt 1020
ggtgacgttt actcgttgca gtcttcaaaa ggggcaacgc caaggacttc taattttgaa 1080
gaggagatgt tgaagatgca caagaagaga ggaggaggga gcatgagtgg cgagttgttt 1140
aatgggggtt tggtttcttc taattaccgc ccaccgaatc caatgttttc agggctacg 1200
agtgtgtgtg gtggcccaa gaagaaagat agcagtgggtg gcggtggtgc tgtagcacct 1260
aacaaggagt tacacatgtt tgtttggagt tcaagtgcac cacctgttcc tgaggggaat 1320
ttgaggcatg cagttaatag agctgcctct actgactttg gaactgtcga tccttctaag 1380
gctgttccac acgaaactgt tgcctcaaaa gctgttcacg aattgattga gaacatgagc 1440
cctggtcgta gagggagtgg agagaggag cctgaaatgg atgaaggagc caaaattccc 1500
gcaagtggat ctccatacac ttgccagaag aaggtggaca tgggaagatg caatgcaaac 1560
aaaaaccaac agatgccacc tgcaagtgtc atgacaagac ttatttctcat catggtttgg 1620
```

```

aggaaactca taagaaatcc taatacttac tccagtcttt tgggactcac atggtctctc 1680
atatcattta ggtggcacat tgaaatgcc aactattgtaa aaggttccat ctcaatactg 1740
tctgatgctg gtctaggaat ggccatgttc agtctagggtc tattcatggc attacaaccg 1800
aagatcattg cctgtggaaa atctgtggca gcattttcaa tggctggttag gttcttgaca 1860
ggtccagctg tgattgctgc aacctcaata ggcacggtac tccgtggagt tcttttgcat 1920
gttgcaattg tccaggtctg tcttcccaa ggtatcggtc cctttgtgtt tgccaaagaa 1980
tacaatctcc atgcagatat acttagcact gcggttata tttgggatgct aattgcattg 2040
cccataacca tactctacta cgtgctgctt ggagttta tttgtcttggg agacaaaagc 2100
aatagaaaaa gaagtatatg ttgctataac tgtacgtact atgtaaacc aatgtcacgc 2160
tcaagcgggg tggatgaagg gaaatgtaga agatattgga ttttagatgt tagagggaaa 2220
gagaaattat atatagtata cggtagaatg ctatatatat taattattta tgattcatat 2280
gaaaattttg gtttgattcg ttccacaaaa aaaaaaaaaa aaaa 2324

```

<210> 34
 <211> 637
 <212> PRT
 <213> Glycine max

<400> 34
 Met Ile Thr Gly Lys Asp Ile Tyr Asp Val Phe Ala Ala Ile Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Lys
 20 25 30
 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Val
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Asp Pro
 50 55 60
 Tyr Ala Met Asn Tyr His Phe Ile Ala Ala Asp Cys Leu Gln Lys Val
 65 70 75 80
 Val Ile Leu Gly Ala Leu Phe Leu Trp Asn Thr Phe Thr Lys His Gly
 85 90 95
 Ser Leu Asp Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Lys Ala Met Tyr Gly Asp Phe
 115 120 125
 Ser Gly Ser Leu Met Val Gln Ile Val Val Leu Gln Ser Val Ile Trp
 130 135 140
 Tyr Thr Leu Met Leu Phe Met Phe Glu Tyr Arg Gly Ala Lys Leu Leu
 145 150 155 160
 Ile Thr Glu Gln Phe Pro Glu Thr Ala Gly Ser Ile Thr Ser Phe Arg
 165 170 175
 Val Asp Ser Asp Val Val Ser Leu Asn Gly Arg Glu Pro Leu Gln Thr
 180 185 190
 Asp Ala Glu Ile Gly Glu Asp Gly Lys Leu His Val Val Val Lys Arg
 195 200 205
 Ser Ala Ala Ser Ser Met Ile Ser Ser Phe Asn Lys Ser His Leu Thr
 210 215 220

Ser Met Thr Pro Arg Ala Ser Asn Leu Thr Gly Val Glu Ile Tyr Ser
 225 230 235 240
 Val Gln Ser Ser Arg Glu Pro Thr Pro Arg Gly Ser Ser Phe Asn Gln
 245 250 255
 Thr Asp Phe Tyr Ala Met Phe Ala Ser Lys Ala Pro Ser Pro Lys His
 260 265 270
 Gly Tyr Thr Asn Ser Phe Gln Ser Asn Asn Gly Gly Ile Gly Asp Val
 275 280 285
 Tyr Ser Leu Gln Ser Ser Lys Gly Ala Thr Pro Arg Thr Ser Asn Phe
 290 295 300
 Glu Glu Glu Met Leu Lys Met His Lys Lys Arg Gly Gly Arg Ser Met
 305 310 315 320
 Ser Gly Glu Leu Phe Asn Gly Gly Leu Val Ser Ser Asn Tyr Pro Pro
 325 330 335
 Pro Asn Pro Met Phe Ser Gly Ser Thr Ser Ala Ala Gly Gly Pro Lys
 340 345 350
 Lys Lys Asp Ser Ser Gly Gly Gly Gly Ala Val Ala Pro Asn Lys Glu
 355 360 365
 Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Gly
 370 375 380
 Asn Leu Arg His Ala Val Asn Arg Ala Ala Ser Thr Asp Phe Gly Thr
 385 390 395 400
 Val Asp Pro Ser Lys Ala Val Pro His Glu Thr Val Ala Ser Lys Ala
 405 410 415
 Val His Glu Leu Ile Glu Asn Met Ser Pro Gly Arg Arg Gly Ser Gly
 420 425 430
 Glu Arg Glu Pro Glu Met Asp Glu Gly Ala Lys Ile Pro Ala Ser Gly
 435 440 445
 Ser Pro Tyr Thr Cys Gln Lys Lys Val Asp Met Glu Asp Gly Asn Ala
 450 455 460
 Asn Lys Asn Gln Gln Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile
 465 470 475 480
 Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser
 485 490 495
 Ser Leu Leu Gly Leu Thr Trp Ser Leu Ile Ser Phe Arg Trp His Ile
 500 505 510
 Glu Met Pro Thr Ile Val Lys Gly Ser Ile Ser Ile Leu Ser Asp Ala
 515 520 525
 Gly Leu Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln
 530 535 540

Pro Lys Ile Ile Ala Cys Gly Lys Ser Val Ala Ala Phe Ser Met Ala
 545 550 555 560

Val Arg Phe Leu Thr Gly Pro Ala Val Ile Ala Ala Thr Ser Ile Gly
 565 570 575

Ile Gly Leu Arg Gly Val Leu Leu His Val Ala Ile Val Gln Ala Ala
 580 585 590

Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Leu
 595 600 605

His Ala Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile Ala
 610 615 620

Leu Pro Ile Thr Ile Leu Tyr Tyr Val Leu Leu Gly Val
 625 630 635

<210> 35
 <211> 473
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (22)

<220>
 <221> unsure
 <222> (46)

<220>
 <221> unsure
 <222> (58)

<220>
 <221> unsure
 <222> (61)

<220>
 <221> unsure
 <222> (91)

<220>
 <221> unsure
 <222> (98)

<220>
 <221> unsure
 <222> (101)

<220>
 <221> unsure
 <222> (122)

<220>
 <221> unsure
 <222> (177)

<220>

<221> unsure

<222> (201)

<220>

<221> unsure

<222> (297)

<220>

<221> unsure

<222> (300) .. (301)

<220>

<221> unsure

<222> (317)

<220>

<221> unsure

<222> (333)

<220>

<221> unsure

<222> (336)

<220>

<221> unsure

<222> (347)

<220>

<221> unsure

<222> (360)

<220>

<221> unsure

<222> (367)

<220>

<221> unsure

<222> (389)

<220>

<221> unsure

<222> (406)

<220>

<221> unsure

<222> (435)

<220>

<221> unsure

<222> (441)

<400> 35

```

cccaccagca gagacgaaga tnccacgagg aaccgttggg atctanctaa ctagctcttc 60
ncgatgatta ccgggaagga catctaccac ntgctggngg nggtggtgcc gctgtacgtg 120
gncatgttca tggcgtacgg gtcggtgcgg tgggtggggca tcttcacgcc ggaccantgc 180
tcgggcatca aacgcttcgt ngccgtcttc gcggtggcgc tcctctcctt ccacttcate 240
tccaccaacg aaccctacgc catggactaa cgcttcctgg gcgccgactc gctgcanaan 300
ntcgttatcc tcgccgncct cgccgtgtgg ganaangtgc tctcccncca acggtgcecn 360

```

WO 00/68389

PCT/US00/12061

ggggganaga aggcggcgaa ggctcctcnc tgggctggga caacanactc ttctccttgg 420
 ggaaagtgcc aaaanactgg ngaaggggaa tccccctgct gggcgcaagt atg 473

<210> 36
 <211> 89
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (10)

<220>
 <221> UNSURE
 <222> (12)..(13)

<220>
 <221> UNSURE
 <222> (20)

<220>
 <221> UNSURE
 <222> (38)

<220>
 <221> UNSURE
 <222> (69)

<220>
 <221> UNSURE
 <222> (78)..(79)..(80)

<220>
 <221> UNSURE
 <222> (85)

<400> 36
 Met Ile Thr Gly Lys Asp Ile Tyr His Xaa Leu Xaa Xaa Val Val Pro
 1 5 10 15

Leu Tyr Val Xaa Met Phe Met Ala Tyr Gly Ser Val Arg Trp Trp Gly
 20 25 30

Ile Phe Thr Pro Asp Xaa Cys Ser Gly Ile Lys Arg Phe Val Ala Val
 35 40 45

Phe Ala Val Ala Leu Leu Ser Phe His Phe Ile Ser Thr Asn Glu Pro
 50 55 60

Tyr Ala Met Asp Xaa Arg Phe Leu Gly Ala Asp Ser Leu Xaa Xaa Xaa
 65 70 75 80

Val Ile Leu Ala Xaa Leu Ala Val Trp
 85

<210> 37
 <211> 2293
 <212> DNA
 <213> Triticum aestivum

<400> 37
 ctggatcgat cccagcagc agagacgaga tcccacgagg aaccgttggg atctagctag 60
 ctactctctc gcgatgatca ccgggaagga catctacgac gtgctggcgg cgggtgggtgcc 120
 gctgtactgt gccatgttca tggcgtagcg gtcggtgcgg tgggtggggca tcttcacgcc 180
 ggaccagtgc tcgggcatca accgcttcgt cgccgtcttc gcggtgcgcg tcctctcctt 240
 ccaacttcac tccaccaacg acccctacgc catggactac cgcttccttg ccgccgactc 300
 gctgcagaag ctctcatcc tcgcccgcct cgccgtgtgg cacaacgtgc tctcccgeta 360
 ccggtgcgcg ggcggcacgg aggcgggcca ggctctctcg ctggactgga ccatcacgct 420
 cttctccctg gcgacgctgc ccaacacgct ggtgatgggc atcccgctgc tgcgcgccat 480
 gtacggcgag ttctcggggg cgctcatggt gcagatcggt gtgctgcaga gcgtcatctg 540
 gtacacgctc atgctcttcc tcttcgagta ccgcggcgcc aaggcgctca tctccgagca 600
 gttcccgcgc gacgtcggcg ccagcatcgc ctcttcctcg gtcgactccg acgtcgtctc 660
 gctcaacggg cgcgaggcgc tgcacgcca cgccgaggtc ggccgcgacg gccgcgtcca 720
 cgctcgtcat cgccgggtcc cgtcgggggt caccacgggc ggccacggcg ccgggcgctc 780
 cgggatctac cgtggcgcggt ccaacgccat gacgccgcgc gcgtccaacc tcacgggcgt 840
 ggagatctac tcgctgcaga cgtcgcggga gccacgcgcg aggcagtcca gcttcaacca 900
 gtccgacttc tactccatgt tcaacgggag caagctgggt agtcccaagg gccagccccc 960
 cgctcgccga ggtgggtggg cgcgcgggca ggggtctgac gagcaggtgg ccaacaagtt 1020
 caaggcgggc gaggcggtg cgccctaccc cgcgcccaac ccgggatga tgcgcggc 1080
 gccacggaag aaggagcttg ggggttccaa ctcaaactcg aacaaggagc tgcacatgtt 1140
 cgtgtggagc tccagcgctg cgcccggtgc ggaggccaac ctccgcaacg ccgtcaacca 1200
 cgccgcgtcc accgacttcg ccgccgcacc gccggcgcca gccacgccac gagacggcgc 1260
 cacaccaga ggcgtgagcg gcagcgtgac gccggtgatg aagaaggacg ccagcagcgg 1320
 cgcggtggag gtggagatcg aggacggcat gatgaagagc ccggcgacgg ggctgggcgc 1380
 caagtccccg gtgtcggggg cccctacgt ggccccgcgg aagaaggggc ccgacgtgcc 1440
 tgggctggag gaggcggcgc acccgatgcc gccggcgagc gtgatgacct ggctcatcct 1500
 catcatggtg tggcgcaagc tcatccgcaa cccaacacc tactccagcc tcatcgccct 1560
 cgtctggtca ctctctctct tcaggtggaa cattcagatg cctacaataa tcaaggggct 1620
 catatccatc ctgtctgatg cagggtatg gatggctatg ttcagcttag gtctcttcat 1680
 ggctctgcaa ccaagatca tctcttgagg gaagtctgtc gccacatttg caatggcagt 1740
 gaggttcttg actgggcggg cgggtgatcg cgcgacctca atcgccgtcg ggctccgggg 1800
 agtgcctcta catgttgcca ttgtccaggc agcacttcca caaggaattg ttccatttgt 1860
 gttcgccaag gactacaatt gccatcctca aatacttagc acagcggtta tttttggaat 1920
 gctcgtggcg ctcccgatca cgatactcta ctacgttctc cttgggatat agattcataa 1980
 tcttgaagaa ccaaggctgc aaatcttcgg gtagggagaa gtagaattct agagagaaaa 2040
 tggcaactga acatgcttgt gggctgtcct gaagacctga agatgcatga gaccaagcag 2100
 aaggataggg agaactaagt aggaccctag acaggaattc aaaggacaga taaagatc 2160
 cttggttcca tttttttaat tttttatatt atttttacta ctgttttaga tccaaagtaa 2220
 aggctagggc tttgagtatg aagagttcaa ccgttaaatc gaaaaaaaaa aaaaaaaaaa 2280
 aaaaaaaaaa aaa 2293

<210> 38
 <211> 632
 <212> PRT
 <213> Triticum aestivum

<400> 38
 Met Ile Thr Gly Lys Asp Ile Tyr Asp Val Leu Ala Ala Val Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Phe Met Ala Tyr Gly Ser Val Arg Trp Trp Gly
 20 25 30
 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Val
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asp Pro
 50 55 60

Tyr Ala Met Asp Tyr Arg Phe Leu Ala Ala Asp Ser Leu Gln Lys Leu
 65 70 75 80
 Val Ile Leu Ala Ala Leu Ala Val Trp His Asn Val Leu Ser Arg Tyr
 85 90 95
 Arg Cys Arg Gly Gly Thr Glu Ala Gly Glu Ala Ser Ser Leu Asp Trp
 100 105 110
 Thr Ile Thr Leu Phe Ser Leu Ala Thr Leu Pro Asn Thr Leu Val Met
 115 120 125
 Gly Ile Pro Leu Leu Arg Ala Met Tyr Gly Asp Phe Ser Gly Ser Leu
 130 135 140
 Met Val Gln Ile Val Val Leu Gln Ser Val Ile Trp Tyr Thr Leu Met
 145 150 155 160
 Leu Phe Leu Phe Glu Tyr Arg Gly Ala Lys Ala Leu Ile Ser Glu Gln
 165 170 175
 Phe Pro Pro Asp Val Gly Ala Ser Ile Ala Ser Phe Arg Val Asp Ser
 180 185 190
 Asp Val Val Ser Leu Asn Gly Arg Glu Ala Leu His Ala Asp Ala Glu
 195 200 205
 Val Gly Arg Asp Gly Arg Val His Val Val Ile Arg Arg Ser Ala Ser
 210 215 220
 Gly Ser Thr Thr Gly Gly His Gly Ala Gly Arg Ser Gly Ile Tyr Arg
 225 230 235 240
 Gly Ala Ser Asn Ala Met Thr Pro Arg Ala Ser Asn Leu Thr Gly Val
 245 250 255
 Glu Ile Tyr Ser Leu Gln Thr Ser Arg Glu Pro Thr Pro Arg Gln Ser
 260 265 270
 Ser Phe Asn Gln Ser Asp Phe Tyr Ser Met Phe Asn Gly Ser Lys Leu
 275 280 285
 Ala Ser Pro Lys Gly Gln Pro Pro Val Ala Gly Gly Gly Gly Ala Arg
 290 295 300
 Gly Gln Gly Leu Asp Glu Gln Val Ala Asn Lys Phe Lys Gly Gly Glu
 305 310 315 320
 Ala Ala Ala Pro Tyr Pro Ala Pro Asn Pro Gly Met Met Met Pro Ala
 325 330 335
 Pro Arg Lys Lys Glu Leu Gly Gly Ser Asn Ser Asn Ser Asp Lys Glu
 340 345 350
 Leu His Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Ala
 355 360 365
 Asn Leu Arg Asn Ala Val Asn His Ala Ala Ser Thr Asp Phe Ala Ala
 370 375 380

Ala Pro Pro Ala Ala Ala Thr Pro Arg Asp Gly Ala Thr Pro Arg Gly
 385 390 395 400
 Val Ser Gly Ser Val Thr Pro Val Met Lys Lys Asp Ala Ser Ser Gly
 405 410 415
 Ala Val Glu Val Glu Ile Glu Asp Gly Met Met Lys Ser Pro Ala Thr
 420 425 430
 Gly Leu Gly Ala Lys Phe Pro Val Ser Gly Ser Pro Tyr Val Ala Pro
 435 440 445
 Arg Lys Lys Gly Ala Asp Val Pro Gly Leu Glu Glu Ala Ala His Pro
 450 455 460
 Met Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp
 465 470 475 480
 Arg Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Ile Gly Leu
 485 490 495
 Val Trp Ser Leu Val Ser Phe Arg Trp Asn Ile Gln Met Pro Thr Ile
 500 505 510
 Ile Lys Gly Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala
 515 520 525
 Met Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Lys Ile Ile Ser
 530 535 540
 Cys Gly Lys Ser Val Ala Thr Phe Ala Met Ala Val Arg Phe Leu Thr
 545 550 555 560
 Gly Pro Ala Val Ile Ala Ala Thr Ser Ile Ala Val Gly Leu Arg Gly
 565 570 575
 Val Leu Leu His Val Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile
 580 585 590
 Val Pro Phe Val Phe Ala Lys Glu Tyr Asn Cys His Pro Gln Ile Leu
 595 600 605
 Ser Thr Ala Val Ile Phe Gly Met Leu Val Ala Leu Pro Ile Thr Ile
 610 615 620
 Leu Tyr Tyr Val Leu Leu Gly Ile
 625 630

<210> 39
 <211> 447
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (366)

<220>
 <221> unsure
 <222> (380)

<220>
 <221> unsure
 <222> (390)

<220>
 <221> unsure
 <222> (418)

<220>
 <221> unsure
 <222> (421)

<220>
 <221> unsure
 <222> (434)

<400> 39
 gcacacagag acagtcatac tactccatca aataagatga tagcgttggg cgacatctac 60
 aagggtggtg aggcgatggc gccgctttac ttcgcgctag ggctcgggta cgggtccgtt 120
 cgatggtggc ggttcttcac ggcgagagcag tgcggcgcca tcaacacgct ggtggtctgc 180
 ttctccatgc ctttcttcac cttcgacttc gtggtccgcg ccgaccccta cgccatgaat 240
 taccggtca tcgccgccga cgccgtcgcc aaacttctcg ccgtgctcgc cgcgcccgtc 300
 tgggcgcgct gcgccaaggc caaggccggc gcctactcgt ggtcatcacg gggttctccc 360
 tgggcncgta caacaacacn ctcgtcgten gggtgccgct tctgggacgc caatttcngg 420
 naattggggg gcanggactt tattttt 447

<210> 40
 <211> 94
 <212> PRT
 <213> Triticum aestivum

<400> 40
 Met Ile Ala Leu Gly Asp Ile Tyr Lys Val Val Glu Ala Met Ala Pro
 1 5 10 15
 Leu Tyr Phe Ala Leu Gly Leu Gly Tyr Gly Ser Val Arg Trp Trp Arg
 20 25 30
 Phe Phe Thr Ala Glu Gln Cys Gly Ala Ile Asn Thr Leu Val Val Cys
 35 40 45
 Phe Ser Met Pro Phe Phe Thr Phe Asp Phe Val Val Arg Ala Asp Pro
 50 55 60
 Tyr Ala Met Asn Tyr Arg Val Ile Ala Ala Asp Ala Val Ala Lys Leu
 65 70 75 80
 Leu Ala Val Leu Ala Ala Ala Val Trp Ala Arg Cys Ala Lys
 85 90

<210> 41
 <211> 415
 <212> DNA
 <213> Triticum aestivum

<400> 41
 ctgcctaaa taaacctctc cccacgcac tccccactc caccacacac cctcaccagc 60
 tcgcccgcag agtgagccga ggccgagagc cggagcgcgga gaggaagaag cagaggaggt 120
 cgggcaagat gatcacgggc acggacttct accacgtgat gacggcggtg gtgccgctgt 180

acgtggccat gatcctcgcc tacggctccg tcaagtgggtg gggcatcttc acgccggacc 240
 agtgctccgg gatcaaccgc ttgctcgcg tcttcgccgt gccgctcttc tccttcact 300
 tcatctccac caacaacccc tacaccatga acctgcgctt catcgccgcc gacacgctgc 360
 agaagctcat gatgctcgcc atgctcaacg cctggagcaa ctctcccgcc gcggc 415

<210> 42
 <211> 91
 <212> PRT
 <213> *Triticum aestivum*

<400> 42
 Met Ile Thr Gly Thr Asp Phe Tyr His Val Met Thr Ala Val Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Gly
 20 25 30
 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro
 50 55 60
 Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Leu
 65 70 75 80
 Met Met Leu Ala Met Leu Asn Ala Trp Ser Asn
 85 90

<210> 43
 <211> 647
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 43
 Met Ile Thr Gly Lys Asp Met Tyr Asp Val Leu Ala Ala Met Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Arg Trp Trp Gly
 20 25 30
 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Val
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Ser Asn Asp Pro
 50 55 60
 Tyr Ala Met Asn Tyr His Phe Leu Ala Ala Asp Ser Leu Gln Lys Val
 65 70 75 80
 Val Ile Leu Ala Ala Leu Phe Leu Trp Gln Ala Phe Ser Arg Arg Gly
 85 90 95
 Ser Leu Glu Trp Met Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Arg Ala Met Tyr Gly Asp Phe
 115 120 125

Ser Gly Asn Leu Met Val Gln Ile Val Val Leu Gln Ser Ile Ile Trp
 130 135 140
 Tyr Thr Leu Met Leu Phe Leu Phe Glu Phe Arg Gly Ala Lys Leu Leu
 145 150 155 160
 Ile Ser Glu Gln Phe Pro Glu Thr Ala Gly Ser Ile Thr Ser Phe Arg
 165 170 175
 Val Asp Ser Asp Val Ile Ser Leu Asn Gly Arg Glu Pro Leu Gln Thr
 180 185 190
 Asp Ala Glu Ile Gly Asp Asp Gly Lys Leu His Val Val Val Arg Arg
 195 200 205
 Ser Ser Ala Ala Ser Ser Met Ile Ser Ser Phe Asn Lys Ser His Gly
 210 215 220
 Gly Gly Leu Asn Ser Ser Met Ile Thr Pro Arg Ala Ser Asn Leu Thr
 225 230 235 240
 Gly Val Glu Ile Tyr Ser Val Gln Ser Ser Arg Glu Pro Thr Pro Arg
 245 250 255
 Ala Ser Ser Phe Asn Gln Thr Asp Phe Tyr Ala Met Phe Asn Ala Ser
 260 265 270
 Lys Ala Pro Ser Pro Arg His Gly Tyr Thr Asn Ser Tyr Gly Gly Ala
 275 280 285
 Gly Ala Gly Pro Gly Gly Asp Val Tyr Ser Leu Gln Ser Ser Lys Gly
 290 295 300
 Val Thr Pro Arg Thr Ser Asn Phe Asp Glu Glu Val Met Lys Thr Ala
 305 310 315 320
 Lys Lys Ala Gly Arg Gly Gly Arg Ser Met Ser Gly Glu Leu Tyr Asn
 325 330 335
 Asn Asn Ser Val Pro Ser Tyr Pro Pro Pro Asn Pro Met Phe Thr Gly
 340 345 350
 Ser Thr Ser Gly Ala Ser Gly Val Lys Lys Lys Glu Ser Gly Gly Gly
 355 360 365
 Gly Ser Gly Gly Gly Val Gly Val Gly Gly Gln Asn Lys Glu Met Asn
 370 375 380
 Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Glu Ala Asn Ala
 385 390 395 400
 Lys Asn Ala Met Thr Arg Gly Ser Ser Thr Asp Val Ser Thr Asp Pro
 405 410 415
 Lys Val Ser Ile Pro Pro His Asp Asn Leu Ala Thr Lys Ala Met Gln
 420 425 430
 Asn Leu Ile Glu Asn Met Ser Pro Gly Arg Lys Gly His Val Glu Met
 435 440 445

Asp Gln Asp Gly Asn Asn Gly Gly Lys Ser Pro Tyr Met Gly Lys Lys
 450 455 460
 Gly Ser Asp Val Glu Asp Gly Gly Pro Gly Pro Arg Lys Gln Gln Met
 465 470 475 480
 Pro Pro Ala Ser Val Met Thr Arg Leu Ile Leu Ile Met Val Trp Arg
 485 490 495
 Lys Leu Ile Arg Asn Pro Asn Thr Tyr Ser Ser Leu Phe Gly Leu Ala
 500 505 510
 Trp Ser Leu Val Ser Phe Lys Trp Asn Ile Lys Met Pro Thr Ile Met
 515 520 525
 Ser Gly Ser Ile Ser Ile Leu Ser Asp Ala Gly Leu Gly Met Ala Met
 530 535 540
 Phe Ser Leu Gly Leu Phe Met Ala Leu Gln Pro Lys Ile Ile Ala Cys
 545 550 555 560
 Gly Lys Ser Val Ala Gly Phe Ala Met Ala Val Arg Phe Leu Thr Gly
 565 570 575
 Pro Ala Val Ile Ala Ala Thr Ser Ile Ala Ile Gly Ile Arg Gly Asp
 580 585 590
 Leu Leu His Ile Ala Ile Val Gln Ala Ala Leu Pro Gln Gly Ile Val
 595 600 605
 Pro Phe Val Phe Ala Lys Glu Tyr Asn Val His Pro Asp Ile Leu Ser
 610 615 620
 Thr Ala Val Ile Phe Gly Met Leu Val Ala Leu Pro Val Thr Val Leu
 625 630 635 640
 Tyr Tyr Val Leu Leu Gly Leu
 645

<210> 44
 <211> 622
 <212> PRT
 <213> Arabidopsis thaliana

<400> 44
 Met Ile Thr Ala Ala Asp Phe Tyr His Val Met Thr Ala Met Val Pro
 1 5 10 15
 Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Lys
 20 25 30
 Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45
 Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ala Ala Asn Asn Pro
 50 55 60
 Tyr Ala Met Asn Leu Arg Phe Leu Ala Ala Asp Ser Leu Gln Lys Val
 65 70 75 80

Ile Val Leu Ser Leu Leu Phe Leu Trp Cys Lys Leu Ser Arg Asn Gly
 85 90 95
 Ser Leu Asp Trp Thr Ile Thr Leu Phe Ser Leu Ser Thr Leu Pro Asn
 100 105 110
 Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly Met Tyr Gly Asn Phe
 115 120 125
 Ser Gly Asp Leu Met Val Gln Ile Val Val Leu Gln Cys Ile Ile Trp
 130 135 140
 Tyr Ile Leu Met Leu Phe Leu Phe Glu Tyr Arg Gly Ala Lys Leu Leu
 145 150 155 160
 Ile Ser Glu Gln Phe Pro Asp Thr Ala Gly Ser Ile Val Ser Ile His
 165 170 175
 Val Asp Ser Asp Ile Met Ser Leu Asp Gly Arg Gln Pro Leu Glu Thr
 180 185 190
 Glu Ala Glu Ile Lys Glu Asp Gly Lys Leu His Val Thr Val Arg Arg
 195 200 205
 Ser Asn Ala Ser Arg Ser Asp Ile Tyr Ser Arg Arg Ser Gln Gly Leu
 210 215 220
 Ser Ala Thr Pro Arg Pro Ser Asn Leu Thr Asn Ala Glu Ile Tyr Ser
 225 230 235 240
 Leu Gln Ser Ser Arg Asn Pro Thr Pro Arg Gly Ser Ser Phe Asn His
 245 250 255
 Thr Asp Phe Tyr Ser Met Met Ala Ser Gly Gly Gly Arg Asn Ser Asn
 260 265 270
 Phe Gly Pro Gly Glu Ala Val Phe Gly Ser Lys Gly Pro Thr Pro Arg
 275 280 285
 Pro Ser Asn Tyr Glu Glu Asp Gly Gly Pro Ala Lys Pro Thr Ala Ala
 290 295 300
 Gly Thr Ala Ala Gly Ala Gly Arg Phe His Tyr Gln Ser Gly Gly Ser
 305 310 315 320
 Gly Gly Gly Gly Gly Ala His Tyr Pro Ala Pro Asn Pro Gly Met Phe
 325 330 335
 Ser Pro Asn Thr Gly Gly Gly Gly Gly Thr Ala Ala Lys Gly Asn Ala
 340 345 350
 Pro Val Val Gly Gly Lys Arg Gln Asp Gly Asn Gly Arg Asp Leu His
 355 360 365
 Met Phe Val Trp Ser Ser Ser Ala Ser Pro Val Ser Asp Val Phe Gly
 370 375 380
 Gly Gly Gly Gly Asn His His Ala Asp Tyr Ser Thr Ala Thr Asn Asp
 385 390 395 400

His Gln Lys Asp Val Lys Ile Ser Val Pro Gln Gly Asn Ser Asn Asp
 405 410 415
 Asn Gln Tyr Val Glu Arg Glu Glu Phe Ser Phe Gly Asn Lys Asp Asp
 420 425 430
 Asp Ser Lys Val Leu Ala Thr Asp Gly Gly Asn Asn Ile Ser Asn Lys
 435 440 445
 Thr Thr Gln Ala Lys Val Met Pro Pro Thr Ser Val Met Thr Arg Leu
 450 455 460
 Ile Leu Ile Met Val Trp Arg Lys Leu Ile Arg Asn Pro Asn Ser Tyr
 465 470 475 480
 Ser Ser Leu Phe Gly Ile Thr Trp Ser Leu Ile Ser Phe Lys Trp Asn
 485 490 495
 Ile Glu Met Pro Ala Leu Ile Ala Lys Ser Ile Ser Ile Leu Ser Asp
 500 505 510
 Ala Gly Leu Gly Met Ala Met Phe Ser Leu Gly Leu Phe Met Ala Leu
 515 520 525
 Asn Pro Arg Ile Ile Ala Cys Gly Asn Arg Arg Ala Ala Phe Ala Ala
 530 535 540
 Ala Met Arg Phe Val Val Gly Pro Ala Val Met Leu Val Ala Ser Tyr
 545 550 555 560
 Ala Val Gly Leu Arg Gly Val Leu Leu His Val Ala Ile Ile Gln Ala
 565 570 575
 Ala Leu Pro Gln Gly Ile Val Pro Phe Val Phe Ala Lys Glu Tyr Asn
 580 585 590
 Val His Pro Asp Ile Leu Ser Thr Ala Val Ile Phe Gly Met Leu Ile
 595 600 605
 Ala Leu Pro Ile Thr Leu Leu Tyr Tyr Ile Leu Leu Gly Leu
 610 615 620

<210> 45
 <211> 425
 <212> DNA
 <213> Triticum aestivum

<400> 45
 gcacgagctc gcctaaataa acctctcccc cacgcactcc cccactccac cacacaccct 60
 caccagctcg cccgcagagt gagccgaggg cgagagccgg agcgcgagag gaagaagcag 120
 aggaggtcgg gcaagatgat cacgggcacg gacttctacc acgtgatgac ggcggtggtg 180
 ccgctgtacg tggccatgat cctcgccctac ggctccgtca agtggtgggg catcttcacg 240
 ccggaccagt gctccgggat caaccgcttc gtcgcgtct tgcgcgtgcc gtcctctctc 300
 ttccacttca tctccaccaa caacccttac accatgaacc tgcgcttcat cgccgccgac 360
 acgtgcaga agctcatgat gctcgccatg ctcaccgcct ggagccacct ctcccgccgc 420
 ggcag 425

<210> 46
 <211> 96

<212> PRT

<213> Triticum aestivum

<400> 46

Met Ile Thr Gly Thr Asp Phe Tyr His Val Met Thr Ala Val Val Pro
 1 5 10 15

Leu Tyr Val Ala Met Ile Leu Ala Tyr Gly Ser Val Lys Trp Trp Gly
 20 25 30

Ile Phe Thr Pro Asp Gln Cys Ser Gly Ile Asn Arg Phe Val Ala Leu
 35 40 45

Phe Ala Val Pro Leu Leu Ser Phe His Phe Ile Ser Thr Asn Asn Pro
 50 55 60

Tyr Thr Met Asn Leu Arg Phe Ile Ala Ala Asp Thr Leu Gln Lys Leu
 65 70 75 80

Met Met Leu Ala Met Leu Thr Ala Trp Ser His Leu Ser Arg Arg Gly
 85 90 95

<210> 47

<211> 855

<212> DNA

<213> Zea mays

<400> 47

ccacgcgtcc ggctgatcgt cctggcgctg ctcaactgcat ggagctacct ctcccgcgcg 60
 ggctgcctcg agtggaccat cacgctcttc tccctgtcga cgctgccc aa cacgctggtg 120
 atgggcatcc cgctgtc aa gggcatgtac ggcgacttct ccggcagcct catggtgcag 180
 atcgtggtgc tccagtgc atcttggtac acgctgatgc tgttcatgtt cgagtaccgc 240
 ggcgccagga tcctcatcac cgagcagttc cccgacacgg cgggcgccat cgcctccatc 300
 gtggtggacc ccgacgtggt gtcgctggac gggcgcaacg acgccatcga gacggaggcc 360
 gaggtgaagg aggacggcaa gatacacgtc accgtgcggc gctccaacgc gtcgcgctcg 420
 gacatctact cccggcggtc catgggggtt tccagcacca cgccgcggcc cagcaacctg 480
 accaacgccg agatctactc gctgcagtcg tcgaggaacc ccacgccgcg gggctccagc 540
 ttcaaccaca ccgacttcta ctccatggtc ggccgcagct ccaacttcgc cgccggggac 600
 gcgttcggcc tgcgcacggg cgccacgccc aggcgtcca actacgagga ggaccgcag 660
 ggcaaggcga acaagtacgg ccagtaccgg gcgccaacc cgccatggc ggcgcagccc 720
 gccaaaggcc tcaagaaggc ggccaatggg caggccaagg gcgaggacgg caaggaccta 780
 cacatgttcg tgtggagctc cagcgcgtcg cccgtgtccg acgtgttcgg caatggcgcc 840
 gccgagtaca acgac 855

<210> 48

<211> 285

<212> PRT

<213> Zea mays

<400> 48

Pro Arg Val Arg Leu Ile Val Leu Ala Leu Leu Thr Ala Trp Ser Tyr
 1 5 10 15

Leu Ser Arg Arg Gly Cys Leu Glu Trp Thr Ile Thr Leu Phe Ser Leu
 20 25 30

Ser Thr Leu Pro Asn Thr Leu Val Met Gly Ile Pro Leu Leu Lys Gly
 35 40 45

WO 00/68389

PCT/US00/12061

Met	Tyr	Gly	Asp	Phe	Ser	Gly	Ser	Leu	Met	Val	Gln	Ile	Val	Val	Leu	
	50					55					60					
Gln	Cys	Ile	Ile	Trp	Tyr	Thr	Leu	Met	Leu	Phe	Met	Phe	Glu	Tyr	Arg	
65					70					75					80	
Gly	Ala	Arg	Ile	Leu	Ile	Thr	Glu	Gln	Phe	Pro	Asp	Thr	Ala	Gly	Ala	
				85					90					95		
Ile	Ala	Ser	Ile	Val	Val	Asp	Pro	Asp	Val	Val	Ser	Leu	Asp	Gly	Arg	
			100					105					110			
Asn	Asp	Ala	Ile	Glu	Thr	Glu	Ala	Glu	Val	Lys	Glu	Asp	Gly	Lys	Ile	
		115					120					125				
His	Val	Thr	Val	Arg	Arg	Ser	Asn	Ala	Ser	Arg	Ser	Asp	Ile	Tyr	Ser	
	130					135					140					
Arg	Arg	Ser	Met	Gly	Phe	Ser	Ser	Thr	Thr	Pro	Arg	Pro	Ser	Asn	Leu	
145				150						155					160	
Thr	Asn	Ala	Glu	Ile	Tyr	Ser	Leu	Gln	Ser	Ser	Arg	Asn	Pro	Thr	Pro	
			165					170						175		
Arg	Gly	Ser	Ser	Phe	Asn	His	Thr	Asp	Phe	Tyr	Ser	Met	Val	Gly	Arg	
			180					185					190			
Ser	Ser	Asn	Phe	Ala	Ala	Gly	Asp	Ala	Phe	Gly	Leu	Arg	Thr	Gly	Ala	
		195					200					205				
Thr	Pro	Arg	Pro	Ser	Asn	Tyr	Glu	Glu	Asp	Pro	Gln	Gly	Lys	Ala	Asn	
	210					215					220					
Lys	Tyr	Gly	Gln	Tyr	Pro	Ala	Pro	Asn	Pro	Ala	Met	Ala	Ala	Gln	Pro	
225					230					235					240	
Ala	Lys	Gly	Leu	Lys	Lys	Ala	Ala	Asn	Gly	Gln	Ala	Lys	Gly	Glu	Asp	
				245					250					255		
Gly	Lys	Asp	Leu	His	Met	Phe	Val	Trp	Ser	Ser	Ser	Ala	Ser	Pro	Val	
			260					265					270			
Ser	Asp	Val	Phe	Gly	Asn	Gly	Ala	Ala	Glu	Tyr	Asn	Asp				
		275					280					285				